

GenCore version 4.5  
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OM protein - protein search, using sw model

Run on: September 10, 2002, 10:44:42 ; Search time 10.35 Seconds  
(without alignments)  
59.856 Million cell updates/sec

Title: US-09-674-254-3

Perfect score: 87

Sequence:

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 105224 seqs, 38719550 residues

Total number of hits satisfying chosen parameters: 105224

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt\_40.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	67	77.0	366	1	LFTB_HUMAN
2	67	77.0	366	1	TGF4_HUMAN
3	66	75.9	368	1	TGF4_MOUSE
4	52	59.8	368	1	LFTB_MOUSE
5	45	51.7	293	1	TRPH_ECOLI
6	44	50.6	293	1	TRPH_SALTY
7	43	49.4	274	1	TRPH_HAEN
8	42	48.3	335	1	HYPB_RHOCA
9	40.5	46.6	351	1	RYPB_XANCP
10	40	46.0	499	1	OPSL_PATYE
11	40	46.0	695	1	SPAL_SYNY3
12	40	46.0	847	1	NIRB_ECOLI
13	40	46.0	1204	1	NOS3_BOVIN
14	39	44.8	248	1	ATPI_PORPU
15	39	44.8	345	1	OCGL_HUMAN
16	39	44.8	448	1	FIBP_ADEP3
17	39	44.8	650	1	Y411_HUMAN
18	38.5	44.3	919	1	NOS3_RAT
19	38.5	44.3	1201	1	NOS3_MOUSE
20	38.5	44.3	1204	1	NOS3_PIG
21	38	43.7	141	1	YM2_DHTV1
22	38	43.7	251	1	ATP6_ANASP
23	38	43.7	351	1	WNT4_HUMAN
24	38	43.7	351	1	WNT4_MOUSE
25	38	43.7	351	1	WNT4_RAT
26	38	43.7	383	1	FLHB_YEREN
27	38	43.7	439	1	P1V2_ADEG1
28	38	43.7	506	1	V152_HPV16
29	38	43.7	825	1	5E5_RAT
30	38	43.7	825	1	LRP_CAEEL
31	37.5	43.1	4753	1	MINC_BACSU
32	37.5	43.1	1202	1	NOS3_HUMAN
33	37	42.5	75	1	COXH_RAT

34 37 42.5 137 1 RL16\_STRPN  
35 37 42.5 140 1 YDAP\_ECOLI  
36 37 42.5 184 1 YTFJ\_ECOLI  
37 37 42.5 219 1 RL10\_BOMMA  
38 37 42.5 233 1 ATPI\_OCHNE  
39 37 42.5 288 1 HEMK\_MYCLE  
40 37 42.5 346 1 TBCC\_HUMAN  
41 37 42.5 395 1 GP44\_HUMAN  
42 37 42.5 659 1 SPA2\_SYNY3  
43 37 42.5 1188 1 YEC5\_YEAST  
44 37 42.5 1331 1 CYAB\_LEIDO  
45 36 41.4 58 1 YBAS\_PHAVU

#### ALIGNMENTS

##### RESULT 1

LFTB\_HUMAN  
ID LFTB\_HUMAN STANDARD; PRT; 366 AA.  
AC 075610;  
DT 16-OCT-2001 (Rel. 40, Created)  
DT 16-OCT-2001 (Rel. 40, Last sequence update)  
DE Left-right determination factor B precursor (Lefty-B protein).  
GN LFTB OR LEFTYB.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Teratocarcinoma;  
RX MEDLINE=99162193; PubMed=10053005;  
RA Kosaki K., Bassi M.T., Kosaki R., Lewin M., Belmont J., Schauer G., Casey B.;  
RT "Characterization and mutation analysis of human LEFTY A and LEFTY B, homologues of murine genes implicated in left-right axis development";  
RL Am. J. Hum. Genet. 64:712-721(1999).  
CC -!- FUNCTION: REQUIRED FOR LEFT-RIGHT ASYMMETRY DETERMINATION OF ORGAN SYSTEMS IN MAMMALS.  
CC -!- SUBCELLULAR LOCATION: Secreted.  
CC -!- PTM: THE PROCESSING OF THE PROTEIN MAY ALSO OCCUR AT THE SECOND R-X-X-R SITE LOCATED AT AA 132-135. PROCESSING APPEARS TO BE REGULATED IN A CELL-TYPE SPECIFIC MANNER.  
CC -!- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.  
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CC -----  
DR EMBL; AF081507; AAC33967.1; JOINED.  
DR EMBL; AF081504; AAC33967.1; JOINED.  
DR EMBL; AF081505; AAC33967.1; JOINED.  
DR EMBL; AF081506; AAC33967.1; JOINED.  
DR EMBL; AF081512; AAD48144.1; JOINED.  
DR HSSP; P10600; ITGJ.  
DR MIM; 603037; .  
DR InterPro; IPR001839; TGF-beta.  
DR InterPro; IPR001111; TGF-beta.  
DR Pfam; PF00019; TGF-beta; 1.  
DR Pfam; PF00688; TGF-beta; 1.  
DR ProDom; PD000357; TGF-beta; 1.  
DR SMART; SM00204; TGF-beta; 1.  
DR PROSITE; PS00250; TGF-beta; 1.  
KW Developmental protein; Growth factor; Cytokine; Glycoprotein; Signal; Multigene family.  
FT SIGNAL 1 21 POTENTIAL.

09x5k1 streptococ  
P76064 escherichia  
P39187 escherichia  
O96647 bombyx mand  
Q40607 ochrosphaer  
P45832 mycobacteri  
Q15814 homo sapien  
Q9y5y4 homo sapien  
P72587 synechocyst  
P39991 saccharomyc  
Q25263 leishmania  
P03939 phaseolus v.

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FT PROPEP      22 76 OR L35 (POTENTIAL).
FT CHAIN       77 366 LEFT-RIGHT DETERMINATION FACTOR B.
FT DISULFID    251 264 BY SIMILARITY.
FT DISULFID    263 316 BY SIMILARITY.
FT DISULFID    293 351 BY SIMILARITY.
FT DISULFID    297 353 BY SIMILARITY.
FT CARBOHYD    158 158 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE    366 AA; 40880 MW; BCF900C71ED9AA2A CRC64;

Query Match      77.0%; Score 67; DB 1; Length 366;
Best Local Similarity 100.0%; Pred. No. 0.00023;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CASDGLVPRRLQ 13
b 353 CASDGLVPRRLQ 365

RESULT 2
TGFA_HUMAN
ID TGFA_HUMAN STANDARD; PRT; 366 AA.
AC O00292; O75611;
DT 01-NOV-1997 (Rel. 35, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 01-MAR-2002 (Rel. 41, Last annotation update)
DE Transforming growth factor beta 4 precursor (TGF-beta 4) (Endometrial
DE bleeding-associated factor) (left-right determination factor A)
DE (Lefty-A protein).
GN EBAF OR TGFb4 OR LEFTA OR LEFTYA.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID:9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Placenta;
RX MEDLINE=97298127; PubMed=9153275;
RA Kothapalli R., Buyuksal I., Wu S.-Q., Chegini N., Tabibzadeh S.;
RT "Detection of eba4, a novel human gene of the transforming growth
RT factor beta superfamily association of gene expression with
RT endometrial bleeding.";
RL J. Clin. Invest. 99:2342-2350(1997).
RN [2]
RP REVISIONS.
RX MEDLINE=99162193; PubMed=10053005;
RA Kothapalli R.;
RL Unpublished results, cited by:
RL Kosaki K., Bassi M.T., Kosaki R., Lewin M., Belmont J., Schauer G.,
RL Casey B.;
RL Am. J. Hum. Genet. 64:712-721(1999).
RN [3]
RP SEQUENCE FROM N.A., AND VARIANT L-R AXIS MALFORMATIONS ASN-342.
RC TISSUE=Placenta;
RX MEDLINE=99162193; PubMed=10053005;
RA Kosaki K., Bassi M.T., Kosaki R., Lewin M., Belmont J., Schauer G.,
RA Casey B.;
RT "Characterization and mutation analysis of human LEFTY A and LEFTY B,
RT homologues of murine genes implicated in left-right axis
RT development.";
RL Am. J. Hum. Genet. 64:712-721(1999).
CC -1- FUNCTION: REQUIRED FOR LEFT-RIGHT ASYMMETRY DETERMINATION OF
CC ORGAN SYSTEMS IN MAMMALS. MAY PLAY A ROLE IN ENDOMETRIAL BLEEDING.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- TISSUE SPECIFICITY: MESENCHYMAL CELLS OF THE ENDOMETRIAL STROMA.
CC -1- DEVELOPMENTAL STAGE: TRANSIENTLY EXPRESSED BEFORE AND DURING
CC MENSTRUAL BLEEDING.
CC -1- PTM: THE PROCESSING OF THE PROTEIN MAY ALSO OCCUR AT THE SECOND R-
CC X-X-R SITE LOCATED AT AA 132-135. PROCESSING APPEARS TO BE
CC REGULATED IN A CELL-TYPE SPECIFIC MANNER.
CC -1- DISEASE: DEFECTS IN EBAF RESULT IN LEFT-RIGHT AXIS MALFORMATIONS
CC INCLUDING LEFT PULMONARY ISOMERISM, CARDIAC ANOMALIES
CC CHARACTERIZED BY COMPLETE ATRIOVENTRICULAR CANAL DEFECT AND

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CC HYPOPLASTIC LEFT VENTRICLE, AND INTERRUPTED INFERIOR VENA CAVA.
CC -1- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.
CC
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CC
CC EMBL; U81523; AAB53269.1; ALT_SEQ.
CC EMBL; AF081511; AAC32600.1; -.
CC EMBL; AF081508; AAC32600.1; JOINED.
CC EMBL; AF081509; AAC32600.1; JOINED.
CC EMBL; AF081510; AAC32600.1; JOINED.
CC EMBL; AF081513; AAD48145.1; -.
CC HSSP; P10600; 1TGJ.
CC MIM; 601877; -.
CC InterPro; IPR001839; TGF-beta.
CC InterPro; IPR001111; TGFb_N.
CC Pfam; PF00019; TGF-beta; 2.
CC Pfam; PF00688; TGFb_propeptide; 1.
CC ProDom; PD000357; TGF-beta; 1.
CC SMART; SM00204; TGFb; 1.
CC PROSITE; PS00250; TGF_BETA_1; 1.
KW Developmental protein; Growth factor; Cytokine; Glycoprotein; Signal;
KW Multigene family; Disease mutation.
FT SIGNAL      1 21 POTENTIAL.
FT PROPEP     22 76 OR L35 (POTENTIAL).
FT CHAIN      77 366 TRANSFORMING GROWTH FACTOR BETA 4.
FT DISULFID   251 264 BY SIMILARITY.
FT DISULFID   263 316 BY SIMILARITY.
FT DISULFID   293 351 BY SIMILARITY.
FT DISULFID   297 353 BY SIMILARITY.
FT CARBOHYD   158 158 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT VARIANT    342 342 S -> N (IN L-R AXIS MALFORMATIONS).
FT SEQUENCE   366 AA; 40920 MW; 63A416CAE30F7A39 CRC64;

Query Match      77.0%; Score 67; DB 1; Length 366;
Best Local Similarity 100.0%; Pred. No. 0.00023;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CASDGLVPRRLQ 13
b 353 CASDGLVPRRLQ 365

RESULT 3
TGFA_MOUSE
ID TGFA_MOUSE STANDARD; PRT; 368 AA.
AC Q64280;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Transforming growth factor beta 4 precursor (TGF-beta 4) (Lefty
DE protein) (Lefty-1 protein) (STRA3 protein).
GN EBAF OR TGFb4 OR STRA3 OR LEFTY OR LEFTY1.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID:10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=96202359; PubMed=8610011;
RA Meno C., Saijoh Y., Fujii H., Ikeda M., Yokoyama T., Yokoyama M.,
RA Toyoda Y., Hamada H.;
RT "Left-right asymmetric expression of the TGF beta-family member lefty
RT in mouse embryos.";
RL Nature 381:151-155(1996).
RN [2]

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Query Match 46.68; Score 40.5; DB 1; Length 351;
Best Local Similarity 71.48; Pred. No. 10;
Matches 10; Conservative 1; Mismatches 2; Indels 1; Gaps 1;

QY 4 DGALVPRRLQ-HRP 16
    I I I I I I I I I I
DB 61 DGALVTRLLQEHQP 74

RESULT 10
OPSL_PATYE
ID OPSL_PATYE STANDARD; PRT; 499 AA.
AC Q15973;
DT 15-JUL-1998 (Rel. 36, Created)
T 15-JUL-1998 (Rel. 36, Last sequence update)
T 30-MAY-2000 (Rel. 39, Last annotation update)
LE Rhodopsin, GQ-coupled (GQ-rhodopsin).
GN SCOP1.
OS Pateinoecten yessoensis (Ezo giant scallop) (Yesso scallop).
OC Eukaryota; Metazoa; Mollusca; Bivalvia; Pteriomorpha; Pectinoida;
OC Pectinoidea; Pectinidae; Pateinoecten.
OX NCBI_TaxID=6573;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE-EYE;
RX MEDLINE=97435252; Pubmed=9287291;
RA Kojima D., Terakita A., Ishikawa T., Tsukahara Y., Maeda A.,
RA Shichida Y.;
RT "A novel Go-mediated phototransduction cascade in scallop visual
RT cells.";
RL J. Biol. Chem. 272:22979-22989(1997).
CC -!- FUNCTION: VISUAL PIGMENTS ARE THE LIGHT-ABSORBING MOLECULES THAT
CC MEDIATE VISION. THEY CONSIST OF AN APOPROTEIN, OPSIN, COVALENTLY
CC LINKED TO CIS-RETINAL.
CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC -!- TISSUE SPECIFICITY: RETINA. EXPRESSED IN THE DEPOLARIZING CELL
CC LAYER OF THE PHOTORECEPTOR CELLS DISTANT FROM THE LENS.
CC -!- PTM: SOME OR ALL OF THE CARBOXYL-TERMINAL SER OR THR RESIDUES MAY
CC BE PHOSPHORYLATED (BY SIMILARITY).
CC -!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
CC OPSIN SUBFAMILY.
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CC -----
CC EMBL; AB006454; BAA22217.1;
CC InterPro; IPR000276; GPCR_Rhodopsn.
CC Pfam; PF0001760; Opsin.
CC Pfam; PF000001; 7tm.1; 1.
CC PRINTS; PR00237; GPCR_Rhodopsn.
CC PROSITE; PS00237; G-PROTEIN_RECEP_FL_1; 1.
CC PROSITE; PS0262; G-PROTEIN_RECEP_FL_2; 1.
CC PROSITE; PS00238; OPSIN; 1.
CC Photoreceptor; Retinal protein; Transmembrane; Glycoprotein; Vision;
KW Phosphorylation; Lipoprotein; Palmitate; G-protein coupled receptor.
FT DOMAIN 1 50 EXTRACELLULAR.
FT TRANSMEM 51 75 1 (POTENTIAL).
FT DOMAIN 76 87 CYTOPLASMIC.
FT TRANSMEM 88 114 2 (POTENTIAL).
FT DOMAIN 115 128 3 (POTENTIAL).
FT TRANSMEM 129 148 4 (POTENTIAL).
FT DOMAIN 149 168 5 (POTENTIAL).
FT TRANSMEM 169 192 6 (POTENTIAL).
FT DOMAIN 193 216 EXTRACELLULAR.
FT TRANSMEM 217 244 5 (POTENTIAL).
FT DOMAIN 245 278 CYTOPLASMIC.
FT TRANSMEM 279 302 6 (POTENTIAL).

Query Match 46.0%; Score 40; DB 1; Length 499;
Best Local Similarity 66.7%; Pred. No. 18;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 8 VPRRLQHRP 16
    I I I I I I I I I I
DB 463 IPRVQHRP 471

RESULT 11
SPAL_SYNY3
ID SPAL_SYNY3 STANDARD; PRT; 695 AA.
AC P74576;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Probable arginine decarboxylase 1 (EC 4.1.1.19) (ADC).
GN SPEAL OR SPEA OR SLR0662.
OS Synechocystis sp. (strain PCC 6803).
OC Bacteria; Cyanobacteria; Chroococcales; Synechocystis.
OX NCBI_TaxID=1148;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=97061201; Pubmed=8905231;
RA Kaneko T., Sato S., Kotani H., Tanaka A., Asamizu E., Nakamura Y.,
RA Miyajima N., Hirosewa M., Sugita M., Sasamoto S., Kimura T.,
RA Hosouchi T., Matsuno A., Muraki A., Nakazaki N., Naruo K., Okumura S.,
RA Shampo S., Takeuchi C., Wada T., Watanabe A., Yasuda M.,
RA Tabata S.;
RT "Sequence analysis of the genome of the unicellular cyanobacterium
RT Synechocystis sp. strain PCC6803. II. Sequence determination of the
RT entire genome and assignment of potential protein-coding regions.";
RL DNA Res. 3:109-136(1996).
CC -!- CATALYTIC ACTIVITY: L-arginine = agmatine + CO(2).
CC -!- COTACTOR: PYRIDOXAL PHOSPHATE (By similarity).
CC -!- PATHWAY: FIRST STEP IN THE BIOSYNTHESIS OF SPERMIDINE FROM
CC ARGinine.
CC -!- SIMILARITY: BELONGS TO FAMILY 2 OF ORNITHINE, DAP, AND ARGinine
CC DECARBOXYLASES.
CC -----
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CC -----
CC EMBL; D90916; BAA18683.1;
CC InterPro; IPR000183; Orn_DAP_Arg_decarboxylase.
CC Pfam; PF02784; Orn_Arg_dec_N; 1.
CC Pfam; PF00278; Orn_DAP_Arg_dec; 2.
CC PRINTS; PR01179; ODADCRBLASE.
CC PROSITE; PS00878; ODR_DC_2.1; 1.
CC PROSITE; PS00879; ODR_DC_2.2; 1.
KW Spermidine biosynthesis; Lyase; Decarboxylase; Pyridoxal phosphate;
KW Complete proteome.
FT DOMAIN 332 342 SUBSTRATE-BINDING (POTENTIAL).
FT TRANSMEM 343 362 5 (POTENTIAL).
FT TRANSMEM 363 382 6 (POTENTIAL).
FT TRANSMEM 383 402 7 (POTENTIAL).
FT TRANSMEM 403 422 8 (POTENTIAL).
FT TRANSMEM 423 442 9 (POTENTIAL).
FT TRANSMEM 443 462 10 (POTENTIAL).
FT TRANSMEM 463 482 11 (POTENTIAL).
FT TRANSMEM 483 502 12 (POTENTIAL).
FT TRANSMEM 503 522 13 (POTENTIAL).
FT TRANSMEM 523 542 14 (POTENTIAL).
FT TRANSMEM 543 562 15 (POTENTIAL).
FT TRANSMEM 563 582 16 (POTENTIAL).
FT TRANSMEM 583 602 17 (POTENTIAL).
FT TRANSMEM 603 622 18 (POTENTIAL).
FT TRANSMEM 623 642 19 (POTENTIAL).
FT TRANSMEM 643 662 20 (POTENTIAL).
FT TRANSMEM 663 682 21 (POTENTIAL).
FT TRANSMEM 683 702 22 (POTENTIAL).
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FT TRANSMEM 763 782 26 (POTENTIAL).
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FT TRANSMEM 1783 1802 77 (POTENTIAL).
FT TRANSMEM 1803 1822 78 (POTENTIAL).
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FT TRANSMEM 1883 1902 82 (POTENTIAL).
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FT TRANSMEM 1923 1942 84 (POTENTIAL).
FT TRANSMEM 1943 1962 85 (POTENTIAL).
FT TRANSMEM 1963 1982 86 (POTENTIAL).
FT TRANSMEM 1983 2002 87 (POTENTIAL).
FT TRANSMEM 2003 2022 88 (POTENTIAL).
FT TRANSMEM 2023 2042 89 (POTENTIAL).
FT TRANSMEM 2043 2062 90 (POTENTIAL).
FT TRANSMEM 2063 2082 91 (POTENTIAL).
FT TRANSMEM 2083 2102 92 (POTENTIAL).
FT TRANSMEM 2103 2122 93 (POTENTIAL).
FT TRANSMEM 2123 2142 94 (POTENTIAL).
FT TRANSMEM 2143 2162 95 (POTENTIAL).
FT TRANSMEM 2163 2182 96 (POTENTIAL).
FT TRANSMEM 2183 2202 97 (POTENTIAL).
FT TRANSMEM 2203 2222 98 (POTENTIAL).
FT TRANSMEM 2223 2242 99 (POTENTIAL).
FT TRANSMEM 2243 2262 100 (POTENTIAL).
FT TRANSMEM 2263 2282 101 (POTENTIAL).
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FT TRANSMEM 2303 2322 103 (POTENTIAL).
FT TRANSMEM 2323 2342 104 (POTENTIAL).
FT TRANSMEM 2343 2362 105 (POTENTIAL).
FT TRANSMEM 2363 2382 106 (POTENTIAL).
FT TRANSMEM 2383 2402 107 (POTENTIAL).
FT TRANSMEM 2403 2422 108 (POTENTIAL).
FT TRANSMEM 2423 2442 109 (POTENTIAL).
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Query Match          46.0%; Score 40; DB 1; Length 695;
Best Local Similarity 72.7%; Pred. No. 26;
Matches 8; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 6 ALVPRRLQHRP 16
DB 208 ALLARRLGHHP 218
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RESULT 12
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AC P08201; STANDARD; PRT; 847 AA.
DT 01-AUG-1988 (Rel. 08, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
T 16-OCT-2001 (Rel. 40, Last annotation update)
JE Nitrite reductase [NAD(P)H] large subunit (EC 1.6.6.4).
GN NIRB OR B3365.
OS Escherichia coli.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Escherichia.
OX NCBI_TaxID=562;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=K12;
RX MEDLINE=89282391; PubMed=2543955;
RA Bell A.I., Gaston K.L., Cole J.A., Busby S.J.W.;
RT "Cloning of binding sequences for the Escherichia coli transcription
RT activators, FNR and CRP: location of bases involved in discrimination
RT between FNR and CRP.";
RL Nucleic Acids Res. 17:3865-3874(1989).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=K12;
RX MEDLINE=90345936; PubMed=2200672;
RA Peakman T., Crouzet J., Mayaux J.F., Busby S.J.W., Mohan S.,
RA Harborne N., Wootton J., Nicolson R., Cole J.A.;
RT "Nucleotide sequence, organisation and structural analysis of the
RT products of genes in the nirB-cysG region of the Escherichia coli
RT K-12 chromosome.";
RL Eur. J. Biochem. 191:315-323(1990).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=K12 / MG155;
RX MEDLINE=97426617; PubMed=9278503;
RA Blattnher F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,
RA Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,
RA Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
RA Mau B., Shao Y.;
RT "The complete genome sequence of Escherichia coli K-12.";
RL Science 277:1453-1474(1997).
RN [4]
RP SEQUENCE OF 1-21 FROM N.A.
RX MEDLINE=88062713; PubMed=2445993;
RA Jayaraman P.S., Peakman T.C., Busby S.J.W., Quincey R.V.,
RA Cole J.A.;
RT "Location and sequence of the promoter of the gene for the NADH-
RT dependent nitrite reductase of Escherichia coli and its regulation by
RT oxygen, the Fnr protein and nitrite.";
RL J. Mol. Biol. 195:781-788(1987).
CC -1- CATALYTIC ACTIVITY: 3 NAD(P)H + nitrite = 3 NAD(P)(+) + NH(4)OH +
CC H(2)O.
CC -1- COFACTOR: THIS ENZYME IS A FAD FLAVOPROTEIN THAT ALSO CONTAINS
CC A SIROHEME AND ONE 2FE-2S IRON-SULFUR CENTER.
CC -1- PATHWAY: SECOND STEP IN NITRATE ASSIMILATION (DENITRIFICATION).
CC -1- SUBUNIT: HOMODIMER WHICH ASSOCIATES WITH NIRD.
CC -1- SIMILARITY: THE C-TERMINAL DOMAIN IS A 4FE-4S/SIROHEME DOMAIN
CC FOUND IN NITRITE REDUCTASES (EC 1.6.6.4 AND EC 1.7.1.1) AND
CC SULFITE REDUCTASES (EC 1.8.1.2 AND EC 1.8.7.1).
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation
CC [3]

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CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; X14202; CA32416.1; -
CC EMBL; U18997; AAA58162.1; -
CC EMBL; AE000412; AAC76390.1; -
CC PIR; S00529; S00529.
CC PIR; S10791; S10791.
CC PIR; S04349; S04349.
CC EcoGene; EG10653; nirB.
CC InterPro; IPR001327; FAD_pyr_redox.
CC InterPro; IPR000660; Nir_Sir.
CC Pfam; PF01077; NIR_SIR; 1.
CC PRINTS; PR00397; SIROHAEM.
CC PROSITE; PS00365; NIR_SIR; 1.
CC Oxidoreductase; FAD; Flavoprotein; Iron-sulfur; Nitrate assimilation;
KW Heme; NADP; Complete proteome.
FT NP_BIND 44 79 FAD (POTENTIAL).
FT METAL 193 225 NAD(P)H (POTENTIAL).
FT METAL 641 641 IRON-SULFUR (2FE-2S) (POTENTIAL).
FT METAL 647 647 IRON-SULFUR (2FE-2S) (POTENTIAL).
FT METAL 681 681 IRON-SULFUR (2FE-2S) (POTENTIAL).
FT METAL 685 685 IRON-SULFUR (2FE-2S) AND SIROHEME
FT (BY SIMILARITY).
FT CONFLICT 442 442 G -> A (IN REF. 1 AND 2).
FT CONFLICT 835 847 YERIPYTLVEDNA -> MNYSQ (IN REF. 1 AND 2).
SQ SEQUENCE 847 AA; 93121 MW; 5265AD93FD390EB4 CRC64;

Query Match          46.0%; Score 40; DB 1; Length 847;
Best Local Similarity 70.0%; Pred. No. 32;
Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 7 LVPRRLQHRP 16
DB 822 MYPREQHRP 831
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RESULT 13
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ID NOS3_BOVIN STANDARD; PRT; 1204 AA.
AC P29473;
DT 01-APR-1993 (Rel. 25, Created)
DT 01-JUL-1993 (Rel. 26, Last sequence update)
DT 01-MAR-2002 (Rel. 41, Last annotation update)
DE Nitric-oxide synthase, endothelial (EC 1.14.13.39) (EC-NOS) (NOS, type
DE III) (NOSIII) (Endothelial NOS) (ENOS) (Constitutive NOS) (CNOS).
GN NOS3.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=92335295; PubMed=1378626;
RA Lamas S., Marsden P.A., Li G.K., Tempst P., Michel T.;
RT "Endothelial nitric oxide synthase: molecular cloning and
RT characterization of a distinct constitutive enzyme isoform.";
RL Proc. Natl. Acad. Sci. U.S.A. 89:6348-6352(1992).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=93055452; PubMed=1385480;
RA Nishida K., Harrison D.G., Navas J.P., Fisher A.A., Dockery S.P.,
RA Tematsu M., Nerem R.M., Alexander R.W., Murphy T.J.;
RT "Molecular cloning and characterization of the constitutive bovine
RT aortic endothelial cell nitric oxide synthase.";
RL J. Clin. Invest. 90:2092-2096(1992).
RN [3]

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RC SEQUENCE FROM N.A.  
 RP TISSUE=Aortic endothelium;  
 RX MEDLINE=92348367; PubMed=1379225;  
 RA Sessa W.C., Harrison J.K., Barber C.M., Zeng D., Durioux M.E.,  
 RA D'Angelo D.D., Lynch K.R., Peach M.J.;  
 RT "Molecular cloning and expression of a cDNA encoding endothelial cell  
 RT nitric oxide synthase.";  
 RL J. Biol. Chem. 267:15274-15276(1992).  
 RN [4]  
 RP MYRISTOYLATION.  
 RX MEDLINE=93231982; PubMed=7682550;  
 RA Busconi L., Michel T.;  
 RT "Endothelial nitric oxide synthase. N-terminal myristoylation  
 RT determines subcellular localization.";  
 RL J. Biol. Chem. 268:8410-8413(1993).  
 RN [5]  
 RP PALMITOYLATION.  
 RX MEDLINE=96102197; PubMed=8524847;  
 RA Robinson L.J., Michel T.;  
 RT "Mutagenesis of palmitoylation sites in endothelial nitric oxide  
 RT synthase identifies a novel motif for dual acylation and subcellular  
 RT targeting.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 92:11776-11780(1995).  
 RN [6]  
 RP X-RAY CRYSTALLOGRAPHY (1.9 ANGSTROMS) OF 66-481.  
 RX MEDLINE=99091052; PubMed=9875848;  
 RA Raman C.S., Li H., Martasek P., Kral V., Masters B.S., Poulos T.L.;  
 RT "Crystal structure of constitutive endothelial nitric oxide synthase:  
 RT a paradigm for pterin function involving a novel metal center.";  
 RL Cell 95:939-950(1998).  
 RN [7]  
 RP X-RAY CRYSTALLOGRAPHY (1.86 ANGSTROMS) OF 66-481.  
 RX MEDLINE=20503854; PubMed=11051558;  
 RA Li H., Raman C.S., Martasek P., Kral V., Masters B.S., Poulos T.L.;  
 RT "Mapping the active site polarity in structures of endothelial  
 RT nitric oxide synthase heme domain complexed with isothioureas.";  
 RL J. Inorg. Biochem. 81:133-139(2000).  
 RN [8]  
 RP X-RAY CRYSTALLOGRAPHY (1.93 ANGSTROMS).  
 RX MEDLINE=21229525; PubMed=11331003;  
 RA Li H., Raman C.S., Martasek P., Masters B.S., Poulos T.L.;  
 RT "Crystallographic studies on endothelial nitric oxide synthase  
 RT complexed with nitric oxide and mechanism-based inhibitors.";  
 RL Biochemistry 40:5399-5406(2001).  
 RN [9]  
 RP X-RAY CRYSTALLOGRAPHY (1.65 ANGSTROMS).  
 RX MEDLINE=21552923; PubMed=11695891;  
 RA Raman C.S., Li H., Martasek P., Southan G., Masters B.S.,  
 RA Poulos T.L.;  
 RT "Crystal structure of nitric oxide synthase bound to nitro indazole  
 RT reveals a novel inactivation mechanism.";  
 RL Biochemistry 40:13448-13455(2001).  
 RN [10]  
 RP X-RAY CRYSTALLOGRAPHY (1.93 ANGSTROMS).  
 RX MEDLINE=21336567; PubMed=11331290;  
 RA Raman C.S., Li H., Martasek P., Babu B.R., Griffith O.W., Southan G.,  
 RA Masters B.S., Poulos T.L.;  
 RT "Implications for isoform-selective inhibitor design derived from the  
 RT binding mode of bulky isothioureas to the heme domain of endothelial  
 RT nitric-oxide synthase.";  
 RL J. Biol. Chem. 276:26486-26491(2001).  
 CC -|- FUNCTION: PRODUCES NITRIC OXIDE (NO) WHICH IS IMPLICATED IN  
 CC VASCULAR SMOOTH MUSCLE RELAXATION THROUGH A CGMP-MEDIATED SIGNAL  
 CC TRANSDUCTION PATHWAY. NO MEDIATES VASCULAR ENDOTHELIAL GROWTH  
 CC FACTOR (VEGF)-INDUCED ANGIOGENESIS IN CORONARY VESSELS AND  
 CC PROMOTES BLOOD CLOTTING THROUGH THE ACTIVATION OF PLATELETS.  
 CC -|- CATALYTIC ACTIVITY: L-arginine + NADPH + H<sup>+</sup> O<sub>2</sub> -> citrulline +  
 CC nitric oxide + NADP(+).  
 CC -|- COFACTOR: HEME. BINDS ONE MOLE EACH OF FAD AND FMN. ALSO REQUIRES  
 CC TETRAHYDROBIOTIN (BH4) WHICH MAY STABILIZE THE DIMERIC FORM OF  
 CC THE ENZYME.  
 CC -|- ENZYME REGULATION: STIMULATED BY CALCIUM/CALMODULIN.  
 CC -|- SUBUNIT: HOMODIMER.

CC -|- SIMILARITY: BELONGS TO THE NOS FAMILY.  
 CC  
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 CC or send an email to license@sib-sib.ch).  
 CC  
 CC EMBL: M99057; AAA30667.1; -  
 CC EMBL: M89952; AAA30494.1; -  
 CC EMBL: M95674; AAA30669.1; -  
 CC DR PDB: 1NSE; 18-MAY-99.  
 CC DR PDB: 2NSE; 23-MAY-99.  
 CC DR PDB: 3NSE; 18-MAY-99.  
 CC DR PDB: 4NSE; 18-MAY-99.  
 CC DR PDB: 8NSE; 21-NOV-01.  
 CC DR PDB: 9NSE; 25-OCT-00.  
 CC DR PDB: 1D1W; 25-OCT-00.  
 CC DR PDB: 1ED4; 23-OCT-00.  
 CC DR PDB: 1DM6; 13-DEC-00.  
 CC DR PDB: 1DM7; 13-DEC-00.  
 CC DR PDB: 1DM8; 13-DEC-00.  
 CC DR PDB: 1DMI; 20-DEC-00.  
 CC DR PDB: 1DMJ; 20-DEC-00.  
 CC DR PDB: 1ED5; 31-JAN-01.  
 CC DR PDB: 1ED6; 31-JAN-01.  
 CC DR PDB: 1FOI; 20-JUL-01.  
 CC DR PDB: 1FOL; 20-JUL-01.  
 CC DR PDB: 1FOO; 20-JUL-01.  
 CC DR PDB: 1FOP; 20-JUL-01.  
 CC DR PDB: 1DIW; 25-JUL-01.  
 CC DR PDB: 1DIY; 25-JUL-01.  
 CC DR PDB: 1D0C; 21-NOV-01.  
 CC DR PDB: 1D0O; 21-NOV-01.  
 CC DR PDB: 1FOJ; 16-NOV-01.  
 CC DR InterPro: IPR003097; FAD\_binding.  
 CC DR InterPro: IPR001094; Flavdn-like.  
 CC DR InterPro: IPR001226; Flavodoxin.  
 CC DR InterPro: IPR001709; Flavpyrid\_cyt\_redctse.  
 CC DR InterPro: IPR004030; NOS.  
 CC DR InterPro: IPR001433; Oxidored\_FAD.  
 CC DR Pfam: PF00667; FAD\_binding; 1.  
 CC DR Pfam: PF00258; flavodoxin; 1.  
 CC DR Pfam: PF00175; NAD\_binding; 1.  
 CC DR Pfam: PF02898; NO\_synthase; 1.  
 CC DR PRINTS: PR00369; FLAVODOXIN.  
 CC DR PRINTS: PR00371; FPNCR.  
 CC DR PROSITE: PS60001; NOS; 1.  
 CC DR Oxidoreductase; NADP; FAD; FMN; Calmodulin-binding; Myristate;  
 CC Lipoprotein; Palmitate; Phosphorylation; Calcium-binding; Heme;  
 CC Zinc; Metal-binding; Multigene family; 3D-structure.  
 CC INIT\_MET 0  
 CC BINDING 185 185  
 CC DOMAIN 491 511  
 CC FT NP\_BIND 650 681  
 CC FT NP\_BIND 794 805  
 CC FT NP\_BIND 936 946  
 CC FT NP\_BIND 1011 1029  
 CC FT NP\_BIND 1109 1124  
 CC FT LIPID 1 1  
 CC FT LIPID 14 14  
 CC FT LIPID 25 25  
 CC FT METAL 95 95  
 CC FT METAL 100 100  
 CC FT MOD\_RES 142 142  
 CC FT CONFLICT 99 99  
 CC FT CONFLICT 164 164  
 CC FT CONFLICT 317 327  
 CC FT CONFLICT 454 454  
 CC FT CONFLICT 458 458  
 CC  
 CC HEME.  
 CC CALMODULIN-BINDING (POTENTIAL).  
 CC FMN (PYRIMIDINE PART) (BY SIMILARITY).  
 CC FAD (ADP PART) (BY SIMILARITY).  
 CC FAD (FLAVIN PART) (BY SIMILARITY).  
 CC NADP (RIBOSE PART) (BY SIMILARITY).  
 CC NADP (ADP PART) (BY SIMILARITY).  
 CC MYRISTATE.  
 CC PALMITATE.  
 CC ZINC.  
 CC ZINC.  
 CC PHOSPHORYLATION (BY CAPK).  
 CC C -> R (IN REF. 3).  
 CC Y -> I (IN REF. 3).  
 CC EHPLEWFAAL -> GAPHTGVVRGP (IN REF. 3).  
 CC S -> Y (IN REF. 3).  
 CC T -> P (IN REF. 3).



FT CONFLICT 740 740 T -> A (IN REF. 3).  
 FT CONFLICT 803 804 CP -> SA (IN REF. 3).  
 FT CONFLICT 856 856 L -> V (IN REF. 3).  
 FT CONFLICT 906 907 WF -> LV (IN REF. 3).  
 FT CONFLICT 1041 1041 A -> H (IN REF. 3).  
 SQ SEQUENCE 1204 AA; 133155 MW; D017210062ABE4B0 CRC64;

Query Match 46.0%; Score 40; DB 1; Length 1204;  
 Best Local Similarity 43.8%; Pred. No. 47;

Matches 7; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

OY 1 CASDGLVPRRLQHRP 16  
 Db 99 CCLGSLVLPKRLQTRP 114

RESULT 14

ATPI\_PORPU  
 ID ATPI\_PORPU STANDARD; PRT; 248 AA.  
 AC P51247;  
 DT 01-OCT-1996 (Rel. 34, Created)  
 DT 01-OCT-1996 (Rel. 34, Last sequence update)  
 DT 01-OCT-1996 (Rel. 34, Last annotation update)  
 DE ATP synthase A chain precursor (EC 3.6.3.14) (Subunit IV).  
 GN ATP.  
 OS Porphyra purpurea.  
 OG Chloroplast.  
 OC Eukaryota; Rhodophyta; Bangiophyceae; Bangiales; Porphyra.  
 OX NCBI\_TaxID=2787;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Reith M.E., Munnolland J.;  
 RT "Complete nucleotide sequence of the Porphyra purpurea chloroplast genome";  
 RL Plant Mol. Biol. Rep. 13:333-335(1995).  
 CC -1- FUNCTION: KEY COMPONENT OF THE PROTON CHANNEL; IT MAY PLAY A DIRECT ROLE IN THE TRANSLLOCATION OF PROTONS ACROSS THE MEMBRANE.  
 CC -1- SUBUNIT: F-TYPE ATPASES HAVE 2 COMPONENTS, CF(1) - THE CATALYTIC CORE - AND CF(0) - THE MEMBRANE PROTON CHANNEL. CF(1) HAS FIVE SUBUNITS: ALPHA(3), BETA(3), GAMMA(1), DELTA(1), EPSILON(1). CF(0) HAS THREE MAIN SUBUNITS: A, B AND C.  
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein. Chloroplast thylakoid membrane.  
 CC -1- SIMILARITY: BELONGS TO THE ATPASE A CHAIN FAMILY.  
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 CC -----  
 DR EMBL; U38804; AAC08133.1; -  
 DR Mendel; 10272; PORPU; atpi.1.  
 DR InterPro; IPR000568; ATP\_synt\_A.  
 DR Pfam; PF00119; ATP\_synt\_A; 1.  
 DR PRINTS; PR00123; ATPASEA.  
 DR PROSITE; PS00449; ATPASE\_A; 1.  
 KW Hydrogen ion transport; CF(0); Chloroplast; Transmembrane; Signal.  
 FT SIGNAL 1 ?  
 FT CHAIN 1 ?  
 FT TRANSMEM 35 55  
 FT TRANSMEM 94 114  
 FT TRANSMEM 133 153  
 FT TRANSMEM 202 222  
 SQ SEQUENCE 248 AA; 27768 MW; 19BF4604B2690169 CRC64;

Query Match 44.8%; Score 39; DB 1; Length 248;  
 Best Local Similarity 50.0%; Pred. No. 13;

Matches 8; Conservative 2; Mismatches 6; Indels 0; Gaps 0;  
 OY 1 CASDGLVPRRLQHRP 16  
 Db 107 CNWAGALIPWKLHLP 122

RESULT 15

OGGI\_HUMAN  
 ID OGGI\_HUMAN STANDARD; PRT; 345 AA.  
 AC O1557; O00390; P78554; O00670; O00705; O14876; O95488; O9UL34;  
 AC Q9Y6C3; Q9Y6C4; Q9UIK0; Q9UIK1; Q9UIK2; Q9Y2C0; Q9Y2C1;  
 DT 16-OCT-2001 (Rel. 40, Created)  
 DT 16-OCT-2001 (Rel. 40, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE N-glycosylase/DNA lyase [Includes: 8-oxoguanine DNA glycosylase  
 DE (EC 3.2.2.-); DNA-(apurinic or apyrimidinic site) lyase  
 DE (EC 4.2.99.18) (AP lyase)].  
 GN OGG1 OR MMH OR MUTM OR OGH1.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A., AND ALTERNATIVE SPLICING.  
 RC TISSUE=Colon;  
 RX MEDLINE=97330655; PubMed=9187114;  
 RA Aburatani H., Hippo Y., Ishida T., Takashima R., Matsuba C.,  
 RA Kodama T., Takao M., Yasui A., Yamamoto K., Asano M., Fukasawa K.,  
 RA Yoshinari T., Inoue H., Otsuka E., Nishimura S.;  
 RT "Cloning and characterization of mammalian 8-hydroxyguanine-specific  
 RT DNA glycosylase/apurinic, apyrimidinic lyase, a functional mutM  
 RT homologue";  
 RL Cancer Res. 57:2151-2156(1997).  
 RN [2]  
 RP SEQUENCE FROM N.A. (ISOFORM 1A).  
 RX MEDLINE=97352815; PubMed=9207108;  
 RA Rosenquist T.A., Zharkov D.O., Grollman A.P.;  
 RT "Cloning and characterization of a mammalian 8-oxoguanine DNA  
 RT glycosylase";  
 RL Proc. Natl. Acad. Sci. U.S.A. 94:7429-7434(1997).  
 RN [3]  
 RP SEQUENCE FROM N.A. (ISOFORM 2).  
 RX MEDLINE=97368311; PubMed=9223306;  
 RA Roldan-Arjona T., Wei Y.-F., Carter K.C., Klungland A., Anselmino C.,  
 RA Wang R.-P., Augustus M., Lindahl T.;  
 RT "Molecular cloning and functional expression of a human cDNA encoding  
 RT the antitumor enzyme 8-hydroxyguanine-DNA glycosylase";  
 RL Proc. Natl. Acad. Sci. U.S.A. 94:8016-8020(1997).  
 RN [4]  
 RP SEQUENCE FROM N.A. (ISOFORM 1A).  
 RX MEDLINE=97368310; PubMed=9223305;  
 RA Radicella J.P., Bherin C., Desmaze C., Fox M.S., Boiteux S.;  
 RT "Cloning and characterization of hOGG1, a human homolog of the OGG1  
 RT gene of Saccharomyces cerevisiae";  
 RL Proc. Natl. Acad. Sci. U.S.A. 94:8010-8015(1997).  
 RN [5]  
 RP SEQUENCE FROM N.A. (ISOFORM 1A).  
 RX MEDLINE=97342862; PubMed=9197244;  
 RA Lu R., Nash H.M., Verdine G.L.;  
 RT "A mammalian DNA repair enzyme that excises oxidatively damaged  
 RT guanines maps to a locus frequently lost in lung cancer";  
 RL Curr. Biol. 7:397-407(1997).  
 RN [6]  
 RP SEQUENCE FROM N.A. (ISOFORM 1A).  
 RX MEDLINE=97334205; PubMed=9190902;  
 RA Arai K., Morishita K., Shimura K., Kohno T., Taniwaki M., Ohwada S.,  
 RA Yokota J.;  
 RT "Cloning of a human homolog of the yeast OGG1 gene that is involved in  
 RT the repair of oxidative DNA damage";  
 RL Oncogene 14:2857-2861(1997).  
 RN [7]  
 RP SEQUENCE FROM N.A. (ISOFORM 1A).

RX MEDLINE=98012228; PubMed=9348312;  
RA Kuo F.C., Sklar J.L.;  
RT "Augmented expression of a human gene for 8-oxoguanine DNA glycosylase  
RT (MutM) in B lymphocytes of the dark zone in lymph node germinal  
RT centers.";  
RL J. Exp. Med. 186:1547-1556(1997).  
RN [8]  
RP SEQUENCE FROM N.A. (ISOFORM 1A).  
RX MEDLINE=98026907; PubMed=9321410;  
RA Bjorås M., Luna L., Johnsen B.E., Hoff E., Haug T., Rognes T.,  
RT Seeborg E.;  
RT "Opposite base-dependent reactions of a human base excision repair  
RT enzyme on DNA containing 7,8-dihydro-8-oxoguanine and abasic sites.";  
RL EMBO J. 16:6314-6322(1997).  
RN [9]  
RP SEQUENCE FROM N.A. (ISOFORM 1A).  
RA Dhenaut A., Boiteux S., Radicella J.;  
RT "Genomic structure and promoter characterization of the human 8-OH-  
RT guanine glycosylase gene (OGG1) gene.";  
RL Submitted (DEC-1998) to the EMBL/GenBank/DBJ databases.  
RN [10]  
RP SEQUENCE FROM N.A., AND ALTERNATIVE SPLICING.  
RX MEDLINE=99380087; PubMed=10449904;  
RA Ishida T., Hippo Y., Nakahori Y., Matsushita I., Kodama T.,  
RT "Structure and chromosome location of human OGG1.";  
RL Cytogenet. Cell Genet. 85:232-236(1999).  
RN [11]  
RP SEQUENCE FROM N.A., AND ALTERNATIVE SPLICING.  
RX MEDLINE=99250167; PubMed=10233168;  
RA Nishioka K., Ohtsubo T., Oda H., Fujiwara T., Kang D., Sugimachi K.,  
RT Nakabeppu Y.;  
RT "Expression and differential intracellular localization of two major  
RT forms of human 8-Oxoguanine DNA glycosylase encoded by alternatively  
RT spliced OGG1 mRNAs.";  
RL Mol. Biol. Cell 10:1637-1652(1999).  
RN [12]  
RP REVIEW.  
RX MEDLINE=20239648; PubMed=10775435;  
RA Boiteux S., Radicella J.P.;  
RT "The human OGG1 gene: structure, functions, and its implication in the  
RT process of carcinogenesis.";  
RL Arch. Biochem. Biophys. 377:1-8(2000).  
RN [13]  
RP VARIANT HIS-154.  
RX MEDLINE=98438755; PubMed=9765618;  
RA Shimura K., Kohno T., Kasai H., Koda K., Sugimura H., Yokota J.;  
RT "Infrequent mutations of the hOGG1 gene, that is involved in the  
RT excision of 8-hydroxyguanine in damaged DNA, in human gastric  
RT cancer.";  
RL Jpn. J. Cancer Res. 89:825-828(1998).  
RN [14]  
RP VARIANT GLN-46.  
RX MEDLINE=98324718; PubMed=9662341;  
RA Chevillard S., Radicella J.P., Levalois C., Lebeau J., Poupon M.F.,  
RT Oudard S., Dutrillaux B., Boiteux S.;  
RT "Mutations in OGG1, a gene involved in the repair of oxidative DNA  
RT damage, are found in human lung and kidney tumours.";  
RL Oncogene 16:3083-3086(1998).  
RN [15]  
RP CHARACTERIZATION OF VARIANT CYS-326.  
RX MEDLINE=99428653; PubMed=10497264;  
RA Dherin C., Radicella J.P., Dizdareglu M., Boiteux S.;  
RT "Excision of oxidatively damaged DNA bases by the human alpha-hOgg1  
RT protein and the polymorphic alpha-hOgg1(Ser326Cys) protein which is  
RT frequently found in human populations.";  
RL Nucleic Acids Res. 27:4001-4007(1999).  
RN [16]  
RP CHARACTERIZATION OF VARIANTS GLN-46; HIS-154 AND CYS-326.  
RX MEDLINE=20368626; PubMed=10908322;  
RA Audebert M., Radicella J.P., Dizdareglu M.;  
RT "Effect of single mutations in the OGG1 gene found in human tumors on  
RT the substrate specificity of the ogg1 protein.";

RL Nucleic Acids Res. 28:2672-2678(2000).  
CC -!- FUNCTION: DNA REPAIR ENZYME THAT INCISES DNA AT 8-OXOG RESIDUES.  
CC EXCISES 7,8-DIHYDRO-8-OXOGUANINE AND 2,6-DIAMINO-4-HYDROXY-5-N-  
CC METHYLFORMAMIDOPRIMIDINE (FAPY) FROM DAMAGED DNA. HAS A BETA-  
CC LASE ACTIVITY THAT NICKS DNA 3' TO THE LESION.  
CC -!- CATALYTIC ACTIVITY: ENDONUCLEOLYTIC CLEAVAGE NEAR APURINIC OR  
CC APYRIMIDINIC SITES TO PRODUCTS WITH 5'-PHOSPHATE.  
CC -!- SUBCELLULAR LOCATION: NUCLEAR (ISOFORM 1A) AND MITOCHONDRIAL  
CC (ISOFORM 2A).  
CC -!- ALTERNATIVE PRODUCTS: 8 ISOFORMS; 1A/ALPHA (SHOWN HERE), 1B, 1C,  
CC 2A/BETA, 2B, 2C, 2D AND 2E; ARE PRODUCED BY ALTERNATIVE SPLICING.  
CC 1A IS THE PREVALENT FORM.  
CC -!- TISSUE SPECIFICITY: UBIQUITOUS.  
CC -!- DISEASE: DEFECTS IN OGG1 ARE ASSOCIATED WITH TUMOR FORMATION.  
CC -!- SIMILARITY: BELONGS TO THE OGG1 FAMILY 1.  
CC  
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CC  
CC EMBL: U96710; AAB81132.1; -;  
CC EMBL: Y11838; CAA72536.1; -;  
CC EMBL: Y11731; CAA72414.1; -;  
CC EMBL: AB000410; BAA19103.1; -;  
CC EMBL: AF003595; AAB61340.1; -;  
CC EMBL: U88527; AAB68614.1; -;  
CC EMBL: U88620; AAB68615.1; -;  
CC EMBL: Y13277; CAA73726.1; -;  
CC EMBL: AF026691; AAB84013.1; -;  
CC EMBL: AJ131341; CAA10351.1; -;  
CC EMBL: AF088282; AAD41680.1; -;  
CC EMBL: AF088282; AAD41681.1; -;  
CC EMBL: AF088282; AAD41682.1; -;  
CC EMBL: AB019528; BAA76635.1; -;  
CC EMBL: AB019529; BAA76636.1; -;  
CC EMBL: AB019530; BAA76637.1; -;  
CC EMBL: AB019531; BAA76638.1; -;  
CC EMBL: AB019532; BAA76639.1; -;  
CC MIM: 601982; -;  
CC InterPro: IPR003265; Endo\_3c.  
CC Pfam: PF00730; HhH-GPD; 1.  
CC  
CC Hydrolase; Nuclease; Endonuclease; Lyase; DNA repair; Glycosidase;  
CC Multifunctional enzyme; Nuclear protein; Mitochondrion;  
CC Alternative splicing; Polymorphism.  
CC ACT\_SITE 249 249 BY SIMILARITY.  
CC VARSPPLIC 317 345 VLFSADLRQSRHQAQEPAPKRRKSGKPEG -> VSVPRCP  
CC (IN ISOFORM 1B).  
CC VARSPPLIC 317 345 VLFSADLRQSRHQAQEPAPKRRKSGKPEG -> TTPSYRCC  
CC SVPTCANPAMLRSHQOASAEVRPKGRKARWGLDKEIFQAPS  
CC PPPTSLSPSPSPSLMLGRGLPVTTSKARHPOIKQSVCTRW  
CC GGGY (IN ISOFORM 1C).  
CC VARSPPLIC 317 345 VLFSADLRQSRHQAQEPAPKRRKSGKPEG -> GLLGNAED  
CC GHQLRLPILFCQHLREGPPPIGRSGOGELEPQLPSLSS  
CC IPYFCDCWTKDQDDPLVTHPSGSRDGHMTQAMPVKVY  
CC SPLATVIGHYMQASLLAL (IN ISOFORM 2A).  
CC VARSPPLIC 250 345 VADICICMLALDKDQPAVPDVMHIAQORDYSWHFTTSQAKG  
CC PSPQNKELNGFERSLWGPVAGAAQVLFASADLRQSRHQA  
CC PPAKRRKSGKPEG -> GLLGNAEDGHQLRLPILFCODHL  
CC REGPPTRGDSQGELEPQLPSLSSLPYGFCDHCWTKDND  
CC  
CC Query Match 44.8%; Score 39; DB 1; Length 345;  
CC Best Local Similarity 70.0%; Pred. No. 19;  
CC Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;  
CC  
CC QY 6 ALVPRRLQHR 15  
CC ||:||: ||  
CC Db 5 ALLPRRMGHR 14

Search completed: September 10, 2002, 10:46:42  
Job time: 120 sec

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OM protein - protein search, using sw model

Run on: September 10, 2002, 10:43:37 ; Search time 15.15 Seconds  
(without alignments)  
101.480 Million cell updates/sec

Title: US-09-674-254-3  
Perfect score: 87  
Sequence: 1 CASDGLVPRRLQHRP 16

Scoring table: BLOSUM62  
Gapop 10.0 , Gapextb\*0.5

Searched: 283138 seqs, 96089334 residues

Total number of hits satisfying chosen parameters: 283138

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database: PIR\_71:\*

- 1: pir1:\*
- 2: pir2:\*
- 3: pir3:\*
- 4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	66	75.9	368	2 S67507	morphogen lefty pr
2	45	51.7	293	2 E64874	probable metal-dep
3	45	51.7	293	2 F90858	probable enzymes
4	45	51.7	293	2 A85761	probable enzymes y
5	44	50.6	293	2 AG0653	conserved hypotet
6	44	50.6	522	2 D81900	hypothetical prote
7	44	50.6	522	2 A81124	conserved hypotet
8	43	49.4	274	2 F64027	hypothetical prote
9	42.5	48.9	656	2 S52262	UV-endonuclease
10	42	48.3	335	2 S38532	hypB protein - Rho
11	41.5	47.7	327	1 S72913	cytochrome c-type
12	41	47.1	606	2 A81219	diol dehydratase-r
13	41	47.1	606	2 AG1572	rfbB homolog - Xan
14	40.5	46.6	351	2 B49906	germin homolog Ger
15	40	46.0	106	2 T09563	dihydropterocae sy
16	40	46.0	289	2 H75511	hypothetical prote
17	40	46.0	335	2 F84411	arginine decarboxy
18	40	46.0	695	2 S76771	nitrite reductase
19	40	46.0	847	2 H31155	nitrite reductase
20	40	46.0	847	2 H65130	nitrite reductase
21	40	46.0	847	2 H65130	nitrite reductase
22	40	46.0	1205	1 A38943	nitric-oxide synth
23	39.5	45.4	262	2 E98265	hypothetical prote
24	39.5	45.4	262	2 A30119	conserved hypotet
25	39	44.8	109	2 T49452	hypothetical prote
26	39	44.8	248	2 S73168	H+-transporting AT
27	39	44.8	346	2 T45069	8-hydroxy-guanine
28	39	44.8	545	2 A87448	conserved hypotet
29	39	44.8	682	2 T28899	hypothetical prote

## ALIGNMENTS

### RESULT 1

S67507  
morphogen lefty precursor - mouse  
C:Species: Mus musculus (house mouse)  
C:Date: 19-Mar-1997 #sequence\_revision 18-Jul-1997 #text\_change 05-Nov-1999  
C:Accession: S67507  
R:Meno, C.; Saijoh, Y.; Fujii, H.; Ikeda, M.; Yokoyama, M.; Toyoda, Y.; Nature 381, 151-155, 1996  
A:Title: Left-right asymmetric expression of the TGF-beta-family member lefty in mouse  
A:Reference number: S67507; MUID:96202359  
A:Accession: S67507  
A:Molecule type: mRNA  
A:Residues: 1-368 <MEN>  
A:Cross-references: EMBL:D83921; NID:91325920; PIDN:BAAL2121.1; PTD:d1012795; PID:g14  
A:Note: the authors translated the codon ACG for residue 241 as His  
C:Keywords: growth factor  
F:78-368/Product: morphogen lefty #status predicted <MAT1>  
F:136-368/Product: morphogen lefty #status predicted <MAT2>

Query Match 75.9%; Score 66; DB 2; Length 368;  
Best Local Similarity 92.3%; Pred. No. 0.00077;  
Matches 12; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 CASDGLVPRRLQ 13  
Db 355 CASDGLVPRRLQ 367  
|||||:|||||

### RESULT 2

E64874  
probable metal-dependent phosphoesterase yciV - Escherichia coli  
C:Species: Escherichia coli  
C:Date: 12-Sep-1997 #sequence\_revision 17-Sep-1997 #text\_change 29-Sep-1999  
C:Accession: E64874  
R:Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.; A.; Rose, D.J.; Mau, B.; Shao, Y.  
Science 277, 1453-1462, 1997  
A:Title: The complete genome sequence of Escherichia coli K-12.  
A:Reference number: A64720; MUID:97426617  
A:Accession: E64874  
A:Status: nucleic acid sequence not shown; translation not shown  
A:Molecule type: DNA  
A:Residues: 1-293 <LAT>  
A:Cross-references: GB:AE000224; GB:U00096; NID:g1787509; PIDN:AAC74348.1; PID:g17875  
A:Experimental source: strain K-12, substrain MG1655  
C:Genetics:  
A:Gene: yciV  
C:Superfamily: hypothetical protein HI1400

Query Match 51.7%; Score 45; DB 2; Length 293;

Best Local Similarity 64.3%; Pred. No. 3.3; Mismatches 0; Gaps 0;

2Y 2 ASDGALVPRRLQHR 15  
 18 ASDGCLTPALVHR 31

RESULT 3  
 F90858  
 probable enzymes [imported] - Escherichia coli (strain O157:H7, substrain R1MD 0509952)  
 C:Species: Escherichia coli  
 C:Date: 18-Jul-2001 #sequence\_revision 18-Jul-2001 #text\_change 03-Aug-2001  
 C:Accession: F90858  
 R:Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C.-G.; Jasanawa, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H.  
 JNA Res. 8, 11-22, 2001  
 A:Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and genomic reference number: A99629; MUID:21156231; PMID:11250796  
 A:Accession: F90858  
 A:Status: preliminary  
 A:Molecule type: DNA  
 A:Residues: 1-293 <HAY>  
 A:Cross-references: GB:BA000007; PIDN:BA035261.1; PID:g13361303; GSPDB:GN00154  
 A:Experimental source: strain O157:H7, substrain R1MD 0509952  
 A:Genetics: ECs1838  
 A:Gene: ECs1838  
 A:Superfamily: hypothetical protein H11400

Query Match 51.7%; Score 45; DB 2; Length 293;  
 Best Local Similarity 64.3%; Pred. No. 3.3; Mismatches 0; Gaps 0;

2Y 2 ASDGALVPRRLQHR 15  
 18 ASDGCLTPALVHR 31

RESULT 4  
 A85761  
 probable enzymes yciI yciV [imported] - Escherichia coli (strain O157:H7, substrain EDL933)  
 C:Species: Escherichia coli  
 C:Date: 16-Feb-2001 #sequence\_revision 16-Feb-2001 #text\_change 14-Sep-2001  
 C:Accession: A85761  
 R:Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayhew, M.W.; Lin, L.; Grobeck, E.J.; Davis, N.W.; Lim, A.; Dialanta, E.; Potamousis, K.; Apodaca, Nature 409, 529-532, 2001  
 A:Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.  
 A:Reference number: A85480; MUID:21074935; PMID:11206551  
 A:Accession: A85761  
 A:Status: preliminary  
 A:Molecule type: DNA  
 A:Residues: 1-293 <STO>  
 A:Cross-references: GB:AE005174; NID:g12515531; PIDN:AA056549.1; GSPDB:GN00145; UMGF:225  
 A:Experimental source: strain O157:H7, substrain EDL933  
 A:Genetics: yciV  
 A:Gene: yciV  
 A:Superfamily: hypothetical protein H11400

Query Match 51.7%; Score 45; DB 2; Length 293;  
 Best Local Similarity 64.3%; Pred. No. 3.3; Mismatches 0; Gaps 0;

2Y 2 ASDGALVPRRLQHR 15  
 18 ASDGCLTPALVHR 31

RESULT 5  
 UG0653  
 conserved hypothetical protein STY1329 [imported] - Salmonella enterica subsp. enterica

C:Species: Salmonella enterica subsp. enterica serovar Typhi  
 A:Note: this species has also been called Salmonella typhi  
 C:Date: 09-Nov-2001 #sequence\_revision 09-Nov-2001 #text\_change 27-Nov-2001  
 C:Accession: AG0653  
 R:Parkhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Church, T.; Connor, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Farr, S.; Moulle, S.; O'Gaora, P.  
 Nature 413, 848-852, 2001  
 A:Authors: Parkhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Church, T.; Connor, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Farr, S.; Moulle, S.; O'Gaora, P.  
 A:Title: Complete genome sequence of a multiple drug resistant Salmonella enterica serovar Typhi  
 A:Reference number: AB0502; PMID:11677608  
 A:Accession: AG0653  
 A:Status: preliminary  
 A:Molecule type: DNA  
 A:Residues: 1-293 <PAR>  
 A:Cross-references: GB:AL513382; PIDN:CAD08410.1; PID:g16502453; GSPDB:GN00176  
 C:Genetics: STY1329  
 A:Gene: STY1329  
 A:Superfamily: hypothetical protein H11400

Query Match 50.6%; Score 44; DB 2; Length 293;  
 Best Local Similarity 64.3%; Pred. No. 5; Mismatches 9; Conservative 0; Indels 5; Gaps 0;

QY 2 ASDGALVPRRLQHR 15  
 18 ASDGCLTPALVHR 31

RESULT 6  
 DB1900  
 hypothetical protein NMA1314 [imported] - Neisseria meningitidis (strain 22491 serogr C:Species: Neisseria meningitidis  
 C:Date: 05-May-2000 #sequence\_revision 05-May-2000 #text\_change 02-Feb-2001  
 C:Accession: DB1900  
 R:Parkhill, J.; Achtman, M.; James, K.D.; Bentley, S.D.; Churcher, C.; Klee, S.R.; Mo, Nature 404, 502-506, 2000  
 A:Title: Complete DNA sequence of a serogroup A strain of Neisseria meningitidis 22491  
 A:Reference number: A81775; MUID:20222556  
 A:Accession: DB1900  
 A:Status: preliminary  
 A:Molecule type: DNA  
 A:Residues: 1-522 <PAR>  
 A:Cross-references: GB:AL162755; GB:AL157959; NID:g7379742; PIDN:CA884566.1; PID:g737  
 A:Experimental source: serogroup A, strain 22491  
 C:Genetics:  
 A:Gene: NMA1314  
 A:Superfamily: Haemophilus influenzae hypothetical protein HI1501

Query Match 50.6%; Score 44; DB 2; Length 522;  
 Best Local Similarity 57.1%; Pred. No. 8.9; Mismatches 8; Conservative 1; Indels 5; Gaps 0;

QY 3 SDGALVPRRLQHR 16  
 143 SDGLYLPNFIHR 156

RESULT 7  
 A81124  
 conserved hypothetical protein NMB1095 [imported] - Neisseria meningitidis (strain MC C:Species: Neisseria meningitidis  
 C:Date: 31-Mar-2000 #sequence\_revision 31-Mar-2000 #text\_change 19-Jan-2001  
 C:Accession: A81124  
 R:Tettelin, H.; Saunders, N.J.; Heidelberg, J.; Jeffries, A.C.; Nelson, K.E.; Eisen, Hickey, E.K.; Haft, D.H.; Salzberg, S.L.; White, O.; Fleischmann, R.D.; Dougherty, B. Science 287, 1809-1815, 2000  
 A:Authors: Grandi, G.; Sun, L.; Smith, H.O.; Fraser, C.M.; Moxon, E.R.; Rappuoli, R.; A:Title: Complete genome sequence of Neisseria meningitidis serogroup B strain MC58.

A:Reference number: A81000; MUID:20175755  
 A:Accession: A81124  
 A:Status: preliminary  
 A:Molecule type: DNA  
 A:Residues: 1-522 <TET>  
 A:Cross-references: GB:AE002459; GB:AE002098; NID:g7226320; PIDN:AAF41487.1; PID:g7226320  
 A:Experimental source: serogroup B, strain MC58  
 C:Genetics:  
 A:Gene: NM81095  
 C:Superfamily: Haemophilus influenzae hypothetical protein H11501

Query Match 50.6%; Score 44; DB 2; Length 522;  
 Best Local Similarity 57.1%; Pred. No. 8.9;  
 Matches 8; Conservative 1; Mismatches 5; Indels 0; Gaps 0;  
 Y 3 SDGALVPRRLQHRP 16  
 III :II III  
 Db 143 SDGLVPRNFIRHP 156

RESULT 8  
 F64027  
 Hypothetical protein H11400 - Haemophilus influenzae (strain Rd KW20)  
 C:Species: Haemophilus influenzae  
 C:Date: 18-Aug-1995 #sequence\_revision 18-Aug-1995 #text\_change 29-Sep-1999  
 C:Accession: F64027  
 R:Fleischmann, R.D.; Adams, M.D.; White, O.; Clayton, R.A.; Kirkness, E.F.; Kerlavage, A.; Gocayne, J.D.; Scott, J.; Shirley, R.; Liu, L.I.; Glodek, A.; Kelley, J.M.; Weidman, J.D.M.; Brandon, R.C.; Fine, L.D.; Fritchman, J.L.; Fuhrmann, J.L.; Geoghagen, N.S.M. Science 269, 496-512, 1995  
 A:Authors: Gnehm, C.L.; McDonald, L.A.; Small, K.V.; Fraser, C.M.; Smith, H.O.; Venter, A.; Title: Whole-genome random sequencing and assembly of Haemophilus influenzae Rd.  
 A:Reference number: A64000; MUID:95350630  
 A:Accession: F64027  
 A:Status: nucleic acid sequence not shown; translation not shown  
 A:Molecule type: DNA  
 A:Residues: 1-274 <TIGR>  
 A:Cross-references: GB:U32820; GB:I42023; NID:g1574231; PIDN:AAC23046.1; PID:g1574235; T  
 C:Superfamily: hypothetical protein H11400

Query Match 49.4%; Score 43; DB 2; Length 274;  
 Best Local Similarity 64.3%; Pred. No. 7;  
 Matches 9; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 2 ASDGALVPRRLQHR 15  
 III :I III  
 Db 13 ASDGVLSPTELVR 26

RESULT 9  
 S55262  
 UV-endonuclease - Neurospora crassa  
 C:Species: Neurospora crassa  
 C:Date: 10-Oct-1995 #sequence\_revision 03-Nov-1995 #text\_change 20-Jun-2000  
 C:Accession: S55262  
 R:Yajima, H.; Takao, M.; Yasuhira, S.; Zhao, J.H.; Ishii, C.; Inoue, H.; Yasui, A. EMBO J. 14, 2393-2399, 1995  
 A:Title: A eukaryotic gene encoding an endonuclease that specifically repairs DNA damage  
 A:Reference number: S55262; MUID:9522980  
 A:Accession: S55262  
 A:Status: nucleic acid sequence not shown  
 A:Molecule type: mRNA  
 A:Residues: 1-656 <YAJ>  
 A:Cross-references: EMBL:D11392; NID:g1526560; PID:g927215  
 C:Genetics:  
 A:Gene: uvel

Query Match 48.9%; Score 42.5; DB 2; Length 656;  
 Best Local Similarity 64.3%; Pred. No. 21;  
 Matches 9; Conservative 2; Mismatches 2; Indels 1; Gaps 1;

QY 4 DGALVPR-RLQHRP 16  
 III :II III  
 Db 495 DGAVTPRRRKHHP 508  
 RESULT 10  
 D38532  
 hypB protein - Rhodobacter capsulatus  
 C:Species: Rhodobacter capsulatus  
 C:Date: 12-Jul-1991 #sequence\_revision 12-Jul-1991 #text\_change 24-Sep-1999  
 C:Accession: D38532; S32950; S21903  
 R:Xu, H.W.; Wall, J.D.  
 J. Bacteriol. 173, 2401-2405, 1991  
 A:Title: Clustering of genes necessary for hydrogen oxidation in Rhodobacter capsulatus  
 A:Reference number: A38532; MUID:91177833  
 A:Accession: D38532  
 A:Status: preliminary  
 A:Molecule type: DNA  
 A:Residues: 1-335 <XUA>  
 A:Cross-references: GB:M55089; NID:g151949; PIDN:AAA72926.1; PID:g151953; EMBL:X61007  
 R:Colbeau, A.; Richaud, P.; Toussaint, B.; Caballero, F.J.; Elster, C.; Delphin, C.; Mol. Microbiol. 8, 15-29, 1993  
 A:Title: Organization of the genes necessary for hydrogenase expression in Rhodobacter  
 A:Reference number: S32941; MUID:93268090  
 A:Accession: S32950  
 A:Status: preliminary; nucleic acid sequence not shown; translation not shown  
 A:Molecule type: DNA  
 A:Residues: 1-335 <COL>  
 A:Cross-references: EMBL:X61007; NID:g46051; PIDN:CAA43326.1; PID:g46053  
 A:Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1991  
 C:Genetics:  
 A:Gene: hypB  
 C:Superfamily: hydrogenase expression/formaton protein hypB

Query Match 48.3%; Score 42; DB 2; Length 335;  
 Best Local Similarity 50.0%; Pred. No. 13;  
 Matches 8; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

QY 1 CASDGLVPRRLQHRP 16  
 III :I III  
 Db 208 CHLDGAMVEQALHLP 223

RESULT 11  
 S72913  
 cytochrome c-type synthesis protein homolog - Mycobacterium leprae  
 N:Alternate names: hypothetical protein B2168\_C3\_281  
 C:Species: Mycobacterium leprae  
 C:Date: 10-Sep-1999 #sequence\_revision 10-Sep-1999 #text\_change 23-Mar-2001  
 C:Accession: S72913  
 R:Smith, D.R.; Robison, K.  
 submitted to the EMBL Data Library, November 1993  
 A:Description: Mycobacterium leprae cosmid B2168.  
 A:Reference number: S72586  
 A:Accession: S72913  
 A:Status: preliminary  
 A:Molecule type: DNA  
 A:Residues: 1-327 <SMT>  
 A:Cross-references: EMBL:U00018; NID:g467037; PIDN:AAA17249.1; PID:g467065  
 C:Superfamily: cytochrome c-type synthesis protein

Query Match 47.7%; Score 41.5; DB 1; Length 327;  
 Best Local Similarity 52.6%; Pred. No. 15;  
 Matches 10; Conservative 3; Mismatches 3; Indels 3; Gaps 1;

QY 1 CASD---GALVPRRLQHRP 16  
 III :II III  
 Db 119 CFSELVAGAVLRRRQYRP 137

```
RESULT 12
AD1219
diol dehydratase-reactivating factor large chain homolog lmoll56 [Imported] - Listeria
Species: Listeria monocytogenes
Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 14-Dec-2001
Accession: AD1219
Glaser, P.; Frangoul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloecker
.; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.; Entian, K.D.; Fsihl, H.
.; Jones, L.M.; Karst, U.
Science 294, 849-852, 2001
Authors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, E.; Maitournam, A.; Ma
.; Schluter, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehland,
Title: Comparative genomics of Listeria species
Reference number: AB1077; MUID:21537279; PMID:11679669
Accession: AD1219
Status: preliminary
Molecule type: DNA
Residues: 1-606 <GLA>
Cross-references: GB:NC_003210; PIDN:CAC99234.1; PID:g16410572; GSPDB:GN00177
Experimental source: strain EGD-e
Genetics:
Gene: lmoll56
Superfamily: Klebsiella oxytoca diol dehydratase-reactivating factor large chain

Query Match 47.1%; Score 41; DB 2; Length 606;
Best Local Similarity 57.1%; Pred. No. 35;
Matches 8; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

Qy 2 ASDGALVPRRLQHR 15
| | | | | | | |
Db 165 ADDGVLVHNRNLHK 178

RESULT 13
AG1572
diol dehydratase-reactivating factor large chain homolog linl120 [Imported] - Listeria
Species: Listeria innocua
Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 14-Dec-2001
Accession: AG1572
Glaser, P.; Frangoul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloecker
.; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.; Entian, K.D.; Fsihl, H.
.; Jones, L.M.; Karst, U.
Science 294, 849-852, 2001
Authors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, E.; Maitournam, A.; Ma
.; Schluter, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehland,
Title: Comparative genomics of Listeria species
Reference number: AB1077; MUID:21537279; PMID:11679669
Accession: AG1572
Status: preliminary
Molecule type: DNA
Residues: 1-606 <GLA>
Cross-references: GB:AL592022; PIDN:CAC96351.1; PID:g164113579; GSPDB:GN00178
Experimental source: strain Cl1pl1262
Genetics:
Gene: linl120
Superfamily: Klebsiella oxytoca diol dehydratase-reactivating factor large chain

Query Match 47.1%; Score 41; DB 2; Length 606;
Best Local Similarity 57.1%; Pred. No. 35;
Matches 8; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

Qy 2 ASDGALVPRRLQHR 15
| | | | | | | |
Db 165 ADDGVLVHNRNLHK 178

RESULT 14
I49906
fbB homolog - Xanthomonas campestris pv. campestris
Species: Xanthomonas campestris pv. campestris
Date: 19-May-1995 #sequence_revision 19-May-1995 #text_change 16-Jul-1999
```

```
C:Accession: B49906
R:Koeplin, R.; Wang, G.; Hoette, B.; Priefer, U.B.; Puehler, A.
J. Bacteriol. 175, 7786-7792, 1993
A:Title: A 3.9-kb DNA region of Xanthomonas campestris pv. campestris that is necessa
A:Reference number: A49906; MUID:94075213
Accession: B49906
Status: preliminary
Molecule type: DNA
Residues: 1-351 <KOE>
Cross-references: GB:L23941; MID:g398116; PIDN:AAA16192.1; PID:g398120
Superfamily: Escherichia coli UDPglucose 4-epimerase; UDPglucose 4-epimerase homolo
F:4-334/Domain: UDPglucose 4-epimerase homology <UDF>

Query Match 46.6%; Score 40.5; DB 2; Length 351;
Best Local Similarity 71.4%; Pred. No. 25;
Matches 10; Conservative 1; Mismatches 2; Indels 1; Gaps 1;

Qy 4 DGALVPRRLQ-HRP 16
| | | | | | | |
Db 61 DGALVTRLQEHQP 74

RESULT 15
T06563
germin homolog Ger4 - wheat (fragment)
Species: Triticum aestivum (common wheat)
Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 20-Jun-2000
Accession: T06563
Bashardes, S.
Submitted to the EMBL Data Library, December 1996
Reference number: Z15759
Accession: T06563
Status: preliminary; translated from GB/EMBL/DDBJ
Molecule type: mRNA
Residues: 1-106 <BAS>
Cross-references: EMBL:Y09918; PIDN:CAA71053.1
Experimental source: germinating embryos
Genetics:
Gene: Ger4
Superfamily: germin
Keywords: cell wall

Query Match 46.0%; Score 40; DB 2; Length 106;
Best Local Similarity 50.0%; Pred. No. 9.1;
Matches 7; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

Qy 1 CASDGAIVPRRLQH 14
| | | | | |
Db 29 CAGETFLIPRLGH 42

Search completed: September 10, 2002, 10:45:54
Job time: 137 sec
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GenCore version 4.5  
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OM protein - protein search, using sw model

Run on: September 10, 2002, 10:40:47 ; Search time 30.11 Seconds  
(without alignments)  
59,023-Million cell updates/sec

Title: US-09-674-254-3  
Perfect score: 87  
Sequence: 1 CASDGLVPRRLQHRP 16

-Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 10.5

Searched: 747574 seqs, 111073796 residues  
Total number of hits satisfying chosen parameters: 747574

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : A\_Geneseq\_032802.\*  
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22: /SIDS1/gcgdata/hold-geneseq/geneseq-emb1/AA2001.DAT.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	87	100.0	16	21	AA198026
2	87	100.0	294	22	AA198026
3	87	100.0	370	21	AA192013
4	67	77.0	120	20	AA193160
5	67	77.0	120	20	AA193159
6	67	77.0	366	20	AA193159
7	67	77.0	366	20	AA193159
8	67	77.0	366	20	AA193159
9	67	77.0	366	20	AA193159
10	67	77.0	366	20	AA193159
11	67	77.0	366	21	AA198575

12	67	77.0	366	22	AA1995157	Human protein seq
13	67	77.0	366	22	AA1995157	PRO317 Homo sapi
14	67	77.0	366	22	AA1995157	Human PRO317 prote
15	67	77.0	366	22	AA1995157	Endometrial bleed
16	66	75.9	368	20	AA193852	Murine lefty prote
17	47	54.0	380	21	AA193852	Neisseria meningit
18	45	51.7	1643	22	AA193852	C glutamicum prote
19	44	50.6	67	20	AA193852	Extended human seq
20	44	50.6	67	21	AA193852	UCK-3 amino acid s
21	44	50.6	67	21	AA193852	Human secreted pro
22	44	50.6	77	19	AA193852	Human secreted pro
23	44	50.6	77	20	AA193852	Human EST encoded
24	44	50.6	77	22	AA193852	Human EST encoded
25	44	50.6	78	19	AA193852	Human secreted pro
26	44	50.6	90	21	AA193852	Human secreted pro
27	44	50.6	99	20	AA193852	Human secreted pro
28	44	50.6	99	21	AA193852	Human secreted pro
29	44	50.6	99	21	AA193852	UCK-1 amino acid s
30	44	50.6	99	21	AA193852	Human protein clon
31	44	50.6	99	22	AA193852	Novel human secret
32	44	50.6	102	16	AA193852	Human secreted pro
33	44	50.6	102	16	AA193852	Hepatitis GB virus
34	44	50.6	102	21	AA193852	Hepatitis GB virus
35	44	50.6	113	22	AA193852	Human colon cancer
36	44	50.6	120	21	AA193852	UCK-4 amino acid s
37	44	50.6	152	20	AA193852	Human PRO772 prote
38	44	50.6	152	21	AA193852	Human PRO772 (UNO
39	44	50.6	152	21	AA193852	Human secreted pro
40	44	50.6	152	21	AA193852	Human secreted pro
41	44	50.6	152	21	AA193852	UCK-2 amino acid s
42	44	50.6	152	21	AA193852	Human transmembran
43	44	50.6	152	22	AA193852	Novel human secret
44	44	50.6	152	22	AA193852	Human secreted pro
45	44	50.6	264	16	AA193852	Hepatitis GB virus

## ALIGNMENTS

RESULT 1  
AA1950826  
ID AA1950826 standard; peptide: 16 AA.  
XX AA1950826;  
AC AC  
DT 18-FEB-2000 (first entry)  
XX  
DE Human ebaf protein antigenic C-terminal peptide.

Antigenic; ebaf; human; fertility; diagnosis; endometrial irregularity;  
endometrial bleeding-associated factor; contraceptive; endometrium;  
fertility-regulating; uterine bleeding; non-receptiveness; marker;  
infertility; conception; in vitro fertilization; artificial insemination  
XX Homo sapiens.  
XX WO9955902-A1.  
XX  
PD 04-NOV-1999.  
XX  
PF 29-APR-1999; 99WO-US09366.  
XX  
PR 29-APR-1998; 98US-0083418.  
XX  
PA (UYSF-) UNIV SOUTH FLORIDA.  
XX  
PI Tablbradeh S;  
XX  
DR WPI; 2000-052811/04.  
XX  
PT Diagnosis of endometrial irregularities by detecting ebaf or its splice  
XX variants, particularly for diagnosing infertility



PS Claim 39; Page 95; 112pp; English.

CC This invention describes a novel method for diagnosing endometrial  
CC irregularities by screening an endometrial sample, or body fluid, for  
CC the presence of eba1 (endometrial bleeding-associated factor) or its  
CC splice variants that are differentially expressed. The product of the  
CC invention has contraceptive and fertility-regulating activity. Eba1 is  
CC associated with natural or abnormal uterine bleeding and is a marker for  
CC non-receptiveness of the endometrium, and is aberrantly expressed in a  
CC subset of infertile women. The method is used for diagnosis, monitoring  
CC and prognosis of infertility, endometriosis and abnormal uterine  
CC bleeding, particularly to determine endometrial receptivity (i.e. for  
CC optimizing the time of conception, including by in vitro fertilization  
CC and artificial insemination methods). Eba1 is also useful as a  
CC contraceptive while agents that down regulate it, e.g. antisense  
CC sequences, are used to treat endometrial disorders, specifically to  
CC restore fertility. This sequence represents an antigenic peptide derived  
CC from the human eba1 protein C-terminal.

XX Sequence 16 AA;

Query Match 100.0%; Score 87; DB 21; Length 16;  
Best Local Similarity 100.0%; Pred. No. 7e-09;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

AY 1 CASDGLVPRRLQHRP 16  
| | | | | | | | | | | | | | | |  
b 1 casdglvprlqhrrp 16

RESULT 2  
AAB35940  
D AAB35940 standard; protein; 294 AA.

XX AAB35940;  
XX 26-FEB-2001 (first entry)  
XX TGF-beta 4 amino acid sequence.

XX Heparin binding; vascular graft; matrix; cell adhesion; growth factor;  
XX wound healing; dermal wound; wound healing; TGF-beta 4.

XX Unidentified.  
XX WO200064481-A1.

XX 02-NOV-2000.  
XX 22-APR-1999; 99WO-IB00800.  
XX 22-APR-1999; 99WO-IB00800.

XX (ETHZ-) ETH ZURICH & UNIV ZURICH.  
XX Sakiyama SE, Hubbell JA;  
XX WPI; 2001-024627/03.

XX Matrix for controlled release of growth factor for wound healing, has  
XX substrate that attaches heparin binding peptide, protein growth factor  
XX that bind heparin with low affinity, and heparin or heparin-like  
XX polymer

XX Example 5; Page 21; 48pp; English.

XX This invention relates to a matrix comprising a substrate capable of  
XX providing attachment of a heparin binding peptide (HBP), a peptide  
XX comprising a binding domain which binds heparin with high affinity,  
XX heparin or heparin-like polymer, and a protein growth factor or peptide  
XX fragment which has a domain that binds heparin with low affinity.  
XX Included in the invention is a vascular graft comprising the matrix,

CC which is capable of supporting cell adhesion. The matrix is used for  
CC delivering low heparin binding affinity growth factor proteins or  
CC peptides in a controlled manner suitable for wound healing. The matrix  
CC can be used in an article for treating dermal wounds, and in an  
CC implantable sterilized composition capable of supporting cell adhesion.  
CC The present sequence represents a growth factor protein. The protein is  
CC used in an example illustrating that non-heparin-binding growth factors  
CC can be released in a controlled manner from heparin-based drug delivery  
CC systems based on their low affinity for heparin.

XX Sequence 294 AA;

Query Match 100.0%; Score 87; DB 22; Length 294;  
Best Local Similarity 100.0%; Pred. No. 1.5e-07;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CASDGLVPRRLQHRP 16  
| | | | | | | | | | | | | | | |  
Db 275 casdglvprlqhrrp 290

RESULT 3  
AAY92013  
ID AAY92013 standard; Protein; 370 AA.

XX AAY92013;  
XX 19-JUL-2000 (first entry)

XX Human transforming growth factor beta 4/ebaf monomer.

XX human transforming growth factor beta 4 monomer; ebaf; CKGF; mutant;  
XX cysteine knot growth factor; hairpin loop; infertility.  
XX Homo sapiens.

XX Key Location/Qualifiers  
XX Misc-difference 1..266  
XX /note= "optionally mutated to increase electrostatic  
XX interaction between beta hairpin structure and  
XX a receptor"

XX Domain 267..287  
XX /label= beta\_hairpin\_loop\_1  
XX /note= "mutant optionally comprises one or more  
XX substitutions in these residues"

XX Misc-difference 288..317  
XX /note= "optionally mutated to increase electrostatic  
XX interaction between beta hairpin structure and  
XX a receptor"

XX Domain 318..337  
XX /label= beta\_hairpin\_loop\_3  
XX /note= "mutant optionally comprises one or more  
XX substitutions in these residues"

XX Misc-difference 338..370  
XX /note= "optionally mutated to increase electrostatic  
XX interaction between beta hairpin structure and  
XX a receptor"

XX WO200017360-A1.

XX 30-MAR-2000.

XX 19-MAR-1999; 99WO-US05908.

XX 22-SEP-1998; 98WO-US19772.

XX (DYMA-) UNIV MARYLAND BALTIMORE.

XX Weintraub BD, Szkudlinski MW;

XX WPI; 2000-283585/24.

OTHER INFORMATION: /note= "Potential proline directed phosphorylation site"  
FEATURE:  
NAME/KEY: Domain  
LOCATION: 97..98  
OTHER INFORMATION: /note= "Potential proline directed phosphorylation site"  
FEATURE:  
NAME/KEY: Domain  
LOCATION: 116..117  
OTHER INFORMATION: /note= "Potential proline directed phosphorylation site"  
FEATURE:  
NAME/KEY: Domain  
LOCATION: 282..283  
OTHER INFORMATION: /note= "Potential proline directed phosphorylation site"  
FEATURE:  
NAME/KEY: Domain  
LOCATION: 459..460  
OTHER INFORMATION: /note= "Potential proline directed phosphorylation site"  
FEATURE:  
NAME/KEY: Domain  
LOCATION: 472..473  
OTHER INFORMATION: /note= "Potential proline directed phosphorylation site"  
FEATURE:  
NAME/KEY: Domain  
LOCATION: 602..603  
OTHER INFORMATION: /note= "Potential proline directed phosphorylation site"  
FEATURE:  
NAME/KEY: Domain  
LOCATION: 727..728  
OTHER INFORMATION: /note= "Potential proline directed phosphorylation site"  
FEATURE:  
NAME/KEY: Domain  
LOCATION: 838..839  
OTHER INFORMATION: /note= "Potential proline directed phosphorylation site"  
FEATURE:  
NAME/KEY: Domain  
LOCATION: 869..870  
OTHER INFORMATION: /note= "Potential proline directed phosphorylation site"  
FEATURE:  
NAME/KEY: Domain  
LOCATION: 872..873  
OTHER INFORMATION: /note= "Potential proline directed phosphorylation site"  
FEATURE:  
NAME/KEY: Domain  
LOCATION: 1085..1086  
OTHER INFORMATION: /note= "Potential proline directed phosphorylation site"  
FEATURE:  
NAME/KEY: Domain  
LOCATION: 1202..1203  
OTHER INFORMATION: /note= "Potential proline directed phosphorylation site"  
FEATURE:  
NAME/KEY: Domain  
LOCATION: 114..116  
OTHER INFORMATION: /note= "cAMP dependent phosphorylation site"  
FEATURE:  
NAME/KEY: Domain  
LOCATION: 141..143  
OTHER INFORMATION: /note= "cAMP dependent phosphorylation site"  
FEATURE:

NAME/KEY: Domain  
LOCATION: 188..170  
OTHER INFORMATION: /note= "cAMP dependent phosphorylation site"  
FEATURE:  
NAME/KEY: Domain  
LOCATION: 633..635  
OTHER INFORMATION: /note= "cAMP dependent phosphorylation site"  
FEATURE:  
NAME/KEY: Domain  
LOCATION: 836..838  
OTHER INFORMATION: /note= "cAMP dependent phosphorylation site"  
FEATURE:  
NAME/KEY: Domain  
LOCATION: 1051..1053  
OTHER INFORMATION: /note= "cAMP dependent phosphorylation site"  
FEATURE:  
NAME/KEY: Domain  
LOCATION: 738..740  
OTHER INFORMATION: /note= "cAMP dependent phosphorylation site"  
US-07-908-245-2

Query Match 46.0%; Score 40; DB 1; Length 1205;  
Best Local Similarity 43.8%; Pred. No. 66;  
Matches 7; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

QY 1 CASDGLVPRRLQHRP 16  
| :||| ||  
DB 100 CCLGSLVLPKRLQTRP 115

RESULT 4  
US-09-428-517-3  
; Sequence 3, Application US/09428517  
; Patent No. 6251636  
; GENERAL INFORMATION:  
; APPLICANT: Betlach, Mary C.  
; APPLICANT: Shah, Sanjay Krishnakant  
; APPLICANT: McDaniel, Robert  
; APPLICANT: Tang, Li  
; TITLE OF INVENTION: RECOMBINANT OLEANDOLIDE POLYKETIDE SYNTHASE  
; FILE REFERENCE: 30062-20029.00  
; CURRENT APPLICATION NUMBER: US/09/428,517  
; CURRENT FILING DATE: 1999-10-28  
; EARLIER APPLICATION NUMBER: 60/120,254  
; EARLIER FILING DATE: 1999-02-16  
; EARLIER APPLICATION NUMBER: 60/106,100  
; EARLIER FILING DATE: 1998-10-29  
; NUMBER OF SEQ ID NOS: 12  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 3  
; LENGTH: 3816  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Recombinant  
; OTHER INFORMATION: Oleandolide PKS  
US-09-428-517-3

Query Match 44.3%; Score 38.5; DB 4; Length 3816;  
Best Local Similarity 45.0%; Pred. No. 4.4e+02;  
Matches 9; Conservative 3; Mismatches 3; Indels 5; Gaps 1;

QY 2 ASDGALVPR-----RLQHRP 16  
|:| | | | :|||  
DB 3586 AADGTLPLLSGLVLRVRRP 3605

RESULT 5  
US-09-067-782A-5  
; Sequence 5, Application US/09067782A  
; Patent No. 6165751  
; GENERAL INFORMATION:  
; APPLICANT: BARNES, MICHAEL  
; TITLE OF INVENTION: NOVEL COMPOUNDS  
; NUMBER OF SEQUENCES: 6  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Ratner & Prestia  
; STREET: P.O. Box 980  
; CITY: Valley Forge  
; STATE: PA  
; COUNTRY: US  
; ZIP: 19482-0980  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: DOS  
; SOFTWARE: FastSeq for Windows Version 2.0  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/067,782A  
; FILING DATE: 28-APR-1998  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: UK 9710734.6  
; FILING DATE: 23-MAY-1997  
; APPLICATION NUMBER: EP 97309144.0  
; FILING DATE: 13-NOV-1998  
; NAME: Prestia, Paul F  
; REGISTRATION NUMBER: 23,031  
; REFERENCE/DOCKET NUMBER: GH-30167  
; TELEPHONE: 601-407-0700  
; TELEFAX: 610-407-0701  
; TELEX: 846169  
; INFORMATION FOR SEQ ID NO: 5:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 121 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; US-09-067-782A-5

Query Match 43.7%; Score 38; DB 4; Length 121;  
Best Local Similarity 57.1%; Pred. No. 12;  
Matches 8; Conservative 1; Mismatches 5; Indels 5; Gaps 0;

Db 3 SDGALVPRRLQHRP 16  
1 ||||| |:  
21 SSRALVPRNAQFKP 34

RESULT 6  
US-09-067-782A-2  
; Sequence 2, Application US/09067782A  
; Patent No. 6165751  
; GENERAL INFORMATION:  
; APPLICANT: BARNES, MICHAEL  
; TITLE OF INVENTION: NOVEL COMPOUNDS  
; NUMBER OF SEQUENCES: 6  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Ratner & Prestia  
; STREET: P.O. Box 980  
; CITY: Valley Forge  
; STATE: PA  
; COUNTRY: US  
; ZIP: 19482-0980  
; COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FastSeq for Windows Version 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/067,782A  
FILING DATE: 28-APR-1998  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: UK 9710734.6  
FILING DATE: 23-MAY-1997  
APPLICATION NUMBER: EP 97309144.0  
FILING DATE: 13-NOV-1998  
ATTORNEY/AGENT INFORMATION:  
NAME: Prestia, Paul F  
REGISTRATION NUMBER: 23,031  
REFERENCE/DOCKET NUMBER: GH-30167  
TELEPHONE: 601-407-0700  
TELEFAX: 610-407-0701  
TELEX: 846169  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 351 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-09-067-782A-2

Query Match 43.7%; Score 38; DB 4; Length 351;  
Best Local Similarity 57.1%; Pred. No. 39;  
Matches 8; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

Qy 3 SDGALVPRRLQHRP 16  
1 ||||| |:  
Db 251 SSRALVPRNAQFKP 264

RESULT 7  
US-09-171-461-32  
; Sequence 32, Application US/09171461  
; Patent No. 6335016  
; GENERAL INFORMATION:  
; APPLICANT: Baker, Adam  
; APPLICANT: Cotten, Matthew  
; APPLICANT: Chiocca, Susanna  
; APPLICANT: Kurzbaue, Robert  
; APPLICANT: Schaffner, Gotthold  
; TITLE OF INVENTION: Chicken Embryo Lethal Orphan (CELO) Virus  
; FILE REFERENCE: 0852.1800000  
; CURRENT APPLICATION NUMBER: US/09/171.461  
; CURRENT FILING DATE: 1999-01-12  
; EARLIER APPLICATION NUMBER: PCT/EP97/01944  
; EARLIER FILING DATE: 1997-04-18  
; NUMBER OF SEQ ID NOS: 54  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 32  
; LENGTH: 439  
; TYPE: PRT  
; ORGANISM: CELO VIRUS  
; FEATURE:  
; OTHER INFORMATION: Position: 5366..6685/Product:IVa2  
US-09-171-461-32

Query Match 43.7%; Score 38; DB 4; Length 439;  
Best Local Similarity 37.5%; Pred. No. 50;  
Matches 6; Conservative 2; Mismatches 8; Indels 0; Gaps 0;

Qy 1 CASDGLVPRRLQHRP 16  
1 ||| : |:  
11

Db 206 CREDGTIAPKTSTFRP 221

## RESULT 8

US-09-300-909-21

; Sequence 21, Application US/09300909

; Patent No. 6306580

; GENERAL INFORMATION:

; APPLICANT:

; TITLE OF INVENTION: PREPARATION OF HUMAN PAPILLOMAVIRUS E1 HAVING

; HELICASE ACTIVITY AND METHOD THEREFOR

; NUMBER OF SEQUENCES: 27

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/300,909

; FILING DATE:

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 60/083,942

; FILING DATE: 01-MAY-1998

; INFORMATION FOR SEQ ID NO: 21:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 506 amino acids

; TYPE: amino acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: protein

; US-09-300-909-21

## Query Match

Best Local Similarity 43.7%; Score 38; DB 4; Length 506;

Matches 8; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY 2 ASDGALVPRRLQHRP 16

|||||:||||

Db 396 ALDGNLVSMDVKHRP 410

## RESULT 9

US-08-472-666-3

; Sequence 3, Application US/08472666

; Patent No. 5821048

; GENERAL INFORMATION:

; APPLICANT: Howley, Peter M.

; APPLICANT: Benson, John D.

; APPLICANT: Yasugi, Toshiharu

; APPLICANT: Sakai, Hiroyuki

; TITLE OF INVENTION: METHOD AND KIT FOR DIAGNOSING

; PAPILLOMAVIRUS-INFECTED CELLS

; NUMBER OF SEQUENCES: 4

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Ann-Louise Kerner, Ph.D.

; ADDRESSEE: Lappin & Kusmer

; STREET: 200 State Street

; CITY: Boston

; STATE: MA

; COUNTRY: USA

; ZIP: 01209

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/472,666

; FILING DATE:

; CLASSIFICATION: 435

; ATTORNEY/AGENT INFORMATION:

; NAME: McDaniels, Patricia A.

; REGISTRATION NUMBER: 33,194

; REFERENCE/DOCKET NUMBER: HAZ-010

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 617-330-1300

; TELEFAX: 617-330-1311

; INFORMATION FOR SEQ ID NO: 3:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 649 amino acids

; TYPE: amino acid

; TOPOLOGY: linear

; MOLECULE TYPE: protein

; ORIGINAL SOURCE:

; ORGANISM: Human papillomavirus-16 E1

; STRAIN: HPV-16

; US-08-472-666-3

## Query Match

Best Local Similarity 43.7%; Score 38; DB 2; Length 649;

Matches 8; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY 2 ASDGALVPRRLQHRP 16

|||||:||||

Db 539 ALDGNLVSMDVKHRP 553

## RESULT 10

PCT-US96-07615-3

; Sequence 3, Application PC/TUS9607615

; GENERAL INFORMATION:

; APPLICANT: PRESIDENT AND FELLOWS OF HARVARD COLLEGE

; TITLE OF INVENTION: METHODS, KITS, AND COMPOSITIONS FOR DIAGNOSING

; PAPILLOMAVIRUS INFECTION

; NUMBER OF SEQUENCES: 4

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Lappin & Kusmer

; STREET: 200 State Street

; CITY: Boston

; STATE: MA

; COUNTRY: USA

; ZIP: 01209

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: PCT/US96/07615

; FILING DATE:

; CLASSIFICATION:

; ATTORNEY/AGENT INFORMATION:

; NAME: Kerner, Ann-Louise

; REGISTRATION NUMBER: 33,523

; REFERENCE/DOCKET NUMBER: HAZ-010PCT

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 617-330-1300

; TELEFAX: 617-330-1311

; INFORMATION FOR SEQ ID NO: 3:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 649 amino acids

; TYPE: amino acid

; TOPOLOGY: linear

; MOLECULE TYPE: protein

; ORIGINAL SOURCE:

; ORGANISM: Human papillomavirus-16 E1

; STRAIN: HPV-16

; PCT-US96-07615-3

## Query Match

Best Local Similarity 43.7%; Score 38; DB 5; Length 649;

Matches 8; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY 2 ASDGALVPRRLQHRP 16  
| | | | : | | |  
Db 539 ALDGNLVSMDVKHRP 553

## RESULT 11

US-08-319-866-10  
; Sequence 10, Application US/08319866  
; Patent No. 5929223  
; GENERAL INFORMATION:  
; APPLICANT: Tully, Timothy P.  
; APPLICANT: Yin, Jerry C.  
; APPLICANT: Regulski, Michael  
; TITLE OF INVENTION: CLONING AND CHARACTERIZATION OF GENES  
; TITLE OF INVENTION: ASSOCIATED WITH LONG-TERM MEMORY  
; NUMBER OF SEQUENCES: 24  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.  
; STREET: Two Militia Drive  
; CITY: Lexington  
; STATE: Massachusetts  
; COUNTRY: USA  
; ZIP: 02173

; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/319,866  
; FILING DATE: 7-OCT-1994  
; CLASSIFICATION: 514  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER:  
; FILING DATE:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Granahan, Patricia  
; REGISTRATION NUMBER: 32,227  
; REFERENCE/DOCKET NUMBER: CSHL94-03  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (617) 861-6240  
; TELEFAX: (617) 861-9540  
; INFORMATION FOR SEQ ID NO: 10:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 1205 amino acids  
; TYPE: amino acid  
; STRANDEDNESS:  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-08-319-866-10

Query Match 43.1%; Score 37.5; DB 2; Length 1205;  
Best Local Similarity 69.2%; Pred. No. 1.9e+02;  
Matches 9; Conservative 2; Mismatches 1; Indels 1; Gaps 1;

QY 5 GALV-PRRLQHRP 16  
| : | | | : | | | |  
Db 103 GSLVLPKRLQTRP 115

## RESULT 12

US-09-123-708-6  
; Sequence 6, Application US/09123708  
; Patent No. 6146887  
; GENERAL INFORMATION:  
; APPLICANT: SCHRADER, Juergen  
; APPLICANT: GOEDECKE, Axel  
; TITLE OF INVENTION: DNA EXPRESSION VECTORS FOR USE IN GENE THERAPEUTIC  
; TITLE OF INVENTION: TREATMENT OF VASCULAR DISORDERS  
; FILE REFERENCE: 511169-2003  
; CURRENT APPLICATION NUMBER: US/09/123,708  
; CURRENT FILING DATE: 1998-07-28

; EARLIER APPLICATION NUMBER: 08/553,503  
; EARLIER FILING DATE: 1996-03-01  
; EARLIER APPLICATION NUMBER: P4411402.8  
; EARLIER FILING DATE: 1994-03-31  
; NUMBER OF SEQ ID NOS: 6  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 6  
; LENGTH: 1205  
; TYPE: PRT  
; ORGANISM: Cytomegalovirus  
US-09-123-708-6

Query Match 43.1%; Score 37.5; DB 4; Length 1205;  
Best Local Similarity 69.2%; Pred. No. 1.9e+02;  
Matches 9; Conservative 2; Mismatches 1; Indels 1; Gaps 1;

QY 5 GALV-PRRLQHRP 16  
| : | | | : | | | |  
Db 103 GSLVLPKRLQTRP 115

## RESULT 13

US-09-123-624-6  
; Sequence 6, Application US/09123624  
; Patent No. 6149936  
; GENERAL INFORMATION:  
; APPLICANT: SCHRADER, Juergen  
; APPLICANT: GOEDECKE, Axel  
; TITLE OF INVENTION: DNA EXPRESSION VECTORS FOR USE IN THE GENE THERAPEUTIC  
; TITLE OF INVENTION: TREATMENT OF VASCULAR DISORDERS  
; FILE REFERENCE: 511169-2004  
; CURRENT APPLICATION NUMBER: US/09/123,624  
; CURRENT FILING DATE: 1998-07-28  
; PRIOR APPLICATION NUMBER: 08/553,503  
; PRIOR FILING DATE: 1996-03-01  
; PRIOR APPLICATION NUMBER: 4411402.8  
; PRIOR FILING DATE: 1994-03-31  
; NUMBER OF SEQ ID NOS: 6  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 6  
; LENGTH: 1205  
; TYPE: PRT  
; ORGANISM: Bos taurus  
US-09-123-624-6

Query Match 43.1%; Score 37.5; DB 4; Length 1205;  
Best Local Similarity 69.2%; Pred. No. 1.9e+02;  
Matches 9; Conservative 2; Mismatches 1; Indels 1; Gaps 1;

QY 5 GALV-PRRLQHRP 16  
| : | | | : | | | |  
Db 103 GSLVLPKRLQTRP 115

## RESULT 14

US-08-858-207A-373  
; Sequence 373, Application US/08858207A  
; Patent No. 6348328  
; GENERAL INFORMATION:  
; APPLICANT: Black, Michael  
; APPLICANT: Hodgson, John  
; APPLICANT: Knowles, David  
; APPLICANT: Nicholas, Richard  
; APPLICANT: Stodola, Robert  
; TITLE OF INVENTION: No. 6348328el Compounds  
; NUMBER OF SEQUENCES: 552  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: SmithKline Beecham Corporation  
; STREET: 709 Swedeland Road  
; CITY: King of Prussia  
; STATE: PA

COUNTRY: USA  
ZIP: 19406-0939  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FastSeq for Windows Version 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/858,207A  
FILING DATE: 09-MAY-1997  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 60/017670  
FILING DATE: 14-MAY-1996  
ATTORNEY/AGENT INFORMATION:  
NAME: Gimmli, Edward R  
REGISTRATION NUMBER: 38,891  
REFERENCE/DOCKET NUMBER: P50475  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 610-270-4478  
TELEFAX: 610-270-5090  
TELEX:  
INFORMATION FOR SEQ ID NO: 373:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 137 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: NO. 6348328e  
US-08-858-207A-373

Query Match 42.5%; Score 37; DB 4; Length 137;  
Best Local Similarity 66.7%; Pred. No. 21;  
Matches 6; Conservative 3; Mismatches 0; Indels 0; Gaps 0;  
QY 7 LVPRRLQHR 15  
DB 2 LVPRVKRHR 10

RESULT 15  
US-08-414-926A-26  
Sequence 26, Application US/08414926A  
Patent No. 5721354  
GENERAL INFORMATION:  
APPLICANT: Spaete, Richard  
APPLICANT: Cha, Tai-An  
TITLE OF INVENTION: NOVEL HUMAN CYTOMEGALOVIRUS  
NUMBER OF SEQUENCES: 27  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Cooley Godward Castro Huddleson & Tatum  
STREET: 5 Palo Alto Square  
CITY: Palo Alto  
STATE: CA  
COUNTRY: USA  
ZIP: 94306-2155  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/414,926A  
FILING DATE: March 31, 1995  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Cseir, Luann  
REGISTRATION NUMBER: 31,822  
REFERENCE/DOCKET NUMBER: AVIR-011/00US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 415-494-7622  
TELEFAX: 415-857-0663

INFORMATION FOR SEQ ID NO: 26:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 336 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
IMMEDIATE SOURCE:  
CLONE: tol.22  
FEATURE:  
NAME/KEY: Protein  
LOCATION: 1..336  
OTHER INFORMATION: /label= UL151  
US-08-414-926A-26

Query Match 42.5%; Score 37; DB 1; Length 336;  
Best Local Similarity 46.7%; Pred. No. 56;  
Matches 7; Conservative 1; Mismatches 7; Indels 0; Gaps 0;  
QY 1 CASDGAIVPRRLQHR 15  
DB 213 CSQHGAFPPARHLHR 227

Search completed: September 10, 2002, 10:45:32  
Job time: 165 sec

GenCore version 4.5  
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: September 10, 2002, 10:42:47 ; Search time 12.84 Seconds  
(without alignments)  
30.437 Million cell updates/sec

Title: US-09-674-254-3  
Perfect score: 87  
Sequence: 1 CASDGLVPRRLQHRP 16

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 231628 seqs, 24425594 residues

Total number of hits satisfying chosen parameters: 231628

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Issued Patents AA:\*  
1: /cgn2\_6/ptodata/2/iaa/5A.COMB.pep:\*  
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3: /cgn2\_6/ptodata/2/iaa/6A.COMB.pep:\*  
4: /cgn2\_6/ptodata/2/iaa/6B.COMB.pep:\*  
5: /cgn2\_6/ptodata/2/iaa/PCTUS.COMB.pep:\*  
6: /cgn2\_6/ptodata/2/iaa/backfiles1.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	67	77.0	366	3	US-08-987-904A-2
2	67	77.0	366	3	US-08-987-904A-4
3	40	46.0	1205	1	US-07-908-245-2
4	38.5	44.3	3816	4	US-09-428-517-3
5	38	43.7	121	4	US-09-067-782A-5
6	38	43.7	351	4	US-09-067-782A-2
7	38	43.7	439	4	US-09-171-461-32
8	38	43.7	506	4	US-09-300-909-21
9	38	43.7	649	2	US-08-472-666-3
10	38	43.7	649	5	PCT-US96-07615-3
11	37.5	43.1	1205	2	US-08-319-866-10
12	37.5	43.1	1205	4	US-09-123-708-6
13	37.5	43.1	1205	4	US-09-123-624-6
14	37	42.5	137	4	US-08-858-207A-373
15	37	42.5	336	1	US-08-414-926A-26
16	37	42.5	336	2	US-08-926-922-26
17	37	42.5	336	3	US-09-253-682-26
18	37	42.5	336	4	US-09-527-657-26
19	37	42.5	395	3	US-08-981-825-6
20	37	42.5	395	4	US-09-480-784-6
21	36	41.4	95	4	US-09-142-078-62
22	36	41.4	95	4	US-09-357-141-62
23	36	41.4	924	2	US-08-588-983-18
24	36	41.4	924	2	US-08-588-976-18
25	36	41.4	2476	2	US-08-276-967-2
26	35	40.2	20	2	US-08-934-915-120
27	35	40.2	255	4	US-09-355-166-3

28	35	40.2	299	4	US-09-286-529-17	Sequence 17, Appl
29	35	40.2	300	2	US-08-794-796-2	Sequence 2, Appl
30	35	40.2	402	1	US-08-460-806-4	Sequence 4, Appl
31	35	40.2	402	1	US-08-460-806-5	Sequence 5, Appl
32	35	40.2	402	1	US-08-325-630-4	Sequence 4, Appl
33	35	40.2	402	1	US-08-325-630-5	Sequence 5, Appl
34	35	40.2	595	2	US-08-677-049-11	Sequence 11, Appl
35	35	40.2	978	2	US-08-415-593-43	Sequence 43, Appl
36	34.5	39.7	1384	4	US-08-976-255-11	Sequence 5, Appl
37	34	39.1	16	1	US-08-307-724B-5	Sequence 5, Appl
38	34	39.1	159	3	US-08-390-353A-5	Sequence 5, Appl
39	34	39.1	173	4	US-09-095-758-7	Sequence 7, Appl
40	34	39.1	173	4	US-09-422-968-7	Sequence 7, Appl
41	34	39.1	175	4	US-09-028-328-4	Sequence 4, Appl
42	34	39.1	210	1	US-08-320-592-4	Sequence 4, Appl
43	34	39.1	210	1	US-08-327-392-4	Sequence 4, Appl
44	34	39.1	210	3	US-08-545-860D-4	Sequence 4, Appl
45	34	39.1	210	5	PCT-US94-04496-4	Sequence 4, Appl

## ALIGNMENTS

RESULT 1

US-08-987-904A-2  
; Sequence 2, Application US/08987904A  
; Patent No. 6027917

; GENERAL INFORMATION:

; APPLICANT: Celeste, Anthony J.

; APPLICANT: Murray, Beth

; TITLE OF INVENTION: BONE MORPHOGENETIC PROTEIN (BMP) - 17 AND BMP-18

; TITLE OF INVENTION: COMPOSITIONS

; NUMBER OF SEQUENCES: 7

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Genetics Institute, Inc.

; STREET: 87 Cambridgepark Drive

; CITY: Cambridge

; STATE: MA

; COUNTRY: US

; ZIP: 02140

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patent In Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/987,904A

; FILING DATE: 10-DEC-1997

; CLASSIFICATION: 435

; ATTORNEY/AGENT INFORMATION:

; NAME: LAZAR, STEVEN R

; REGISTRATION NUMBER: 32,618

; REFERENCE/DOCKET NUMBER: GI 5307

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (617) 498-8769

; TELEFAX: (617) 876-8581

; INFORMATION FOR SEQ ID NO: 2:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 366 amino acids

; TYPE: amino acid

; TOPOLOGY: linear

; MOLECULE TYPE: protein

US-08-987-904A-2

Query Match 77.0%; Score 67; DB 3; Length 366;  
Best Local Similarity 100.0%; Pred. No. 0.00024;  
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 CASDGLVPRRLQ 13

Db 353 CASDGLVPRRLQ 365

```

RESULT 2
US-08-987-904A-4
; Sequence 4, Application US/08987904A
; Patent No. 6027917
; GENERAL INFORMATION:
; APPLICANT: Celeste, Anthony J.
; APPLICANT: Murray, Beth
; TITLE OF INVENTION: BONE MORPHOGENETIC PROTEIN (BMP)- 17 AND BMP-18
; TITLE OF INVENTION: COMPOSITIONS
; NUMBER OF SEQUENCES: 7
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genetics Institute, Inc.
; STREET: 87 CambridgePark Drive
; CITY: Cambridge
; STATE: MA
; COUNTRY: US
; ZIP: 02140
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/987,904A
; FILING DATE: 10-DEC-1997
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: LAZAR, STEVEN R
; REGISTRATION/DOCKET NUMBER: 32,618
; REFERENCE/DOCKET NUMBER: GI 5307
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 498-8769
; TELEFAX: (617) 876-8581
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 366 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-987-904A-4

Query Match 77.0%; Score 67; DB 3; Length 366;
Best Local Similarity 100.0%; Pred. No. 0.00024;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CASDGLVPRRLQ 13
| | | | | | | | | | | | | | |
Db 353 CASDGLVPRRLQ 365

3ULT 3
; -07-908-245-2
; Sequence 2, Application US/07908245
; Patent No. 5498539
; GENERAL INFORMATION:
; APPLICANT: Harrison, David G.
; APPLICANT: Alexander, R. Wayne
; APPLICANT: Murphy, T.J.
; APPLICANT: Nishida, Ken'ichi
; TITLE OF INVENTION: Endothelial Nitric Oxide Synthase
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Kilpatrick & Cody
; STREET: 1100 Peachtree Street, Suite 2800
; CITY: Atlanta
; STATE: Georgia
; COUNTRY: U.S.
; ZIP: 30309-4530
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible

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; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/908,245
; FILING DATE: 19920702
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Pabst, Patrea L.
; REGISTRATION/DOCKET NUMBER: 31,284
; REFERENCE/DOCKET NUMBER: EMU 111
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 404-815-6508
; TELEFAX: 404-815-6555
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1205 amino acids
; TYPE: AMINO ACID
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE: N-terminal
; ORIGINAL SOURCE:
; ORGANISM: Bovine
; TISSUE TYPE: Aorta
; CELL TYPE: Endothelial
; FEATURE:
; NAME/KEY: Binding-site
; LOCATION: 496..512
; OTHER INFORMATION: /note= "CA++/CAM binding domain"
; FEATURE:
; NAME/KEY: Binding-site
; LOCATION: 651..678
; OTHER INFORMATION: /note= "FMN binding domain"
; FEATURE:
; NAME/KEY: Binding-site
; LOCATION: 795..806
; OTHER INFORMATION: /note= "FAD-Pyrophosphate binding
; OTHER INFORMATION: domain"
; FEATURE:
; NAME/KEY: Binding-site
; LOCATION: 937..947
; OTHER INFORMATION: /note= "FAD-Isolalloxanthine
; OTHER INFORMATION: binding domain"
; FEATURE:
; NAME/KEY: Binding-site
; LOCATION: 1012..1030
; OTHER INFORMATION: /note= "NADPH-Ribose binding
; OTHER INFORMATION: domain"
; FEATURE:
; NAME/KEY: Binding-site
; LOCATION: 1111..1124
; OTHER INFORMATION: /note= "NADPH-Ribose binding
; OTHER INFORMATION: domain"
; FEATURE:
; NAME/KEY: Domain
; LOCATION: 33..34
; OTHER INFORMATION: /note= "Potential proline directed
; OTHER INFORMATION: phosphorylation site"
; FEATURE:
; NAME/KEY: Domain
; LOCATION: 46..47
; OTHER INFORMATION: /note= "Potential proline directed
; OTHER INFORMATION: phosphorylation site"
; FEATURE:
; NAME/KEY: Domain
; LOCATION: 53..54
; OTHER INFORMATION: /note= "Potential proline directed
; OTHER INFORMATION: phosphorylation site"
; FEATURE:
; NAME/KEY: Domain
; LOCATION: 58..59

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PT	New mutant cysteine knot growth factor proteins comprising one or more
PT	mutant subunits, useful for treating or preventing diseases e.g.
PT	hypothyroidism and thyroid cancer
XX	
PS	Claim 238; Page 302; 320pp; English.
XX	
CC	This is the wild type human transforming growth factor beta 4 monomer.
CC	Mutants comprise at least one electrostatic charge altering mutation in a
CC	beta hairpin loop, resulting in increased bioactivity.
CC	Mutant cysteine knot growth factor (CKGF) proteins comprising one or more
CC	mutant subunits and having novel properties or improved pharmacological
CC	properties, compared to wild type CKGFs, are claimed. The CKGF
CC	superfamily comprises at least four families of growth factors: the
CC	glycoprotein hormones, the platelet-derived growth factor (PDGF) family,
CC	the neurotrophins and the transforming growth factor-beta family; the
CC	families are known to be structurally similar (especially comprising the
CC	cysteine knot topology) and it was shown that mutations at certain
CC	positions in the CKGF hairpin loops of family members and other members
CC	of the CKGF superfamily could significantly alter the biological
CC	activities of the CKGF.
CC	Mutant transforming growth factor family proteins or analogues are useful
CC	for treatment of ovulatory dysfunction, luteal phase defect, unexplained
CC	infertility, time-limited conception and in assisted reproduction.
XX	
SQ	Sequence 370 AA;

```

Query Match      100.0%; Score 87; DB 21; Length 370;
Best Local Similarity 100.0%; Pred. No. 1.9e-07;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 CASD GALVPRRLQHRP 16
      |||||
Db      351 casd galvprrlqhrp 366

RESULT      4
AAW93160
ID      AAW93160 standard; Protein; 120 AA.
XX
AC      AAW93160;
XX
DT      21-MAY-1999 (first entry)
XX
DE      Human Lefty-2 protein fragment.
XX
KW      Lefty-2; human; growth differentiation factor; detection; ovarian; colon;
treatment; cell proliferative disorder; immunological disorder; disease;
muscle; muscledegenerative disorder; tissue repair; burn; contraceptive;
premature labour; fetal growth; cancer; gonadal; adrenal; tumour;
endometrial.
XX
OS      Homo sapiens.
XX
PN      WO9906443-AL.
XX
PD      11-FEB-1999.
XX
PF      24-JUL-1998; 98WO-US15174.
XX
PR      31-JUL-1997; 97US-0054381.
XX
      (UYJO ) UNIV JOHNS HOPKINS SCHOOL MEDICINE.
XX
      Huynh TV, Lee S, Sebald S;
PI
XX
DR      WPI; 1999-153703/13.
XX
DR      N-PSDB; AAX22359.
XX
PT      A new growth differentiation factor, Lefty-2 - useful to detect and
treat cell proliferative and immunological disorders
XX
PS      Example 1; Fig 1; 38pp; English.

```

```

XX This sequence represents a novel human growth differentiation factor,
CC Lefty-2. Molecules of the invention may be used to detect or treat cell
CC proliferative or immunological disorders, including disease processes
CC involving muscle such as musclogenenerative disorders or tissue repair
CC following trauma or burns, in contraceptive regimens, to prevent
CC premature labour, to enhance fetal growth or development, or to treat
CC various cancers including gonadal and adrenal tumours, endometrial and
CC ovarian tumours and colon cancer.
XX
SQ Sequence 120 AA;

Query Match 77.0%; Score 67; DB 20; Length 120;
Best Local Similarity 100.0%; Pred No. 0.00024;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 CASDGLVPRRLQ L3
Db 107 casdglvprrlq 119
|||||

RESULT 5
AAW93159
ID AAW93159 standard; Protein; 120 AA.
XX
XX AC AAW93159;
XX
XX 21-MAY-1999 (first entry)
XX
XX Human Lefty-1 protein fragment.
XX
XX Lefty-1; human; growth differentiation factor; detection; ovarian; colon
XX treatment; cell proliferative disorder; immunological disorder; disease;
XX muscle; musclogenenerative disorder; tissue repair; burn; contraceptive
XX premature labour; fetal growth; cancer; gonadal; adrenal; tumour;
XX endometrial.
XX
XX Homo sapiens.
XX
XX OS
XX
XX PN WO9906444-A1.
XX
XX PD 11-FEB-1999.
XX
XX PF 24-JUL-1998; 98WO-US15352.
XX
XX PR 31-JUL-1997; 97US-0054382.
XX
XX PA (UWJO ) UNIV JOHNS HOPKINS SCHOOL MEDICINE.
XX
XX PI Huynh TV, Lee S, Sebald S;
XX
XX DR WPI; 1999-153704/13.
XX
XX DR N-PSDB; AAX22358.
XX
XX
XX A new growth differentiation factor, Lefty-1 - useful to detect and
XX treat cell proliferative and immunological disorders
XX
XX Example 1; Figure 1; 38pp; English.
XX
XX This sequence represents a novel human growth differentiation factor,
XX Lefty-1. The polynucleotides, proteins and antibodies described in the
XX invention may be used to detect or treat cell proliferative or
XX immunological disorders, including disease processes involving muscle
XX such as musclogenenerative disorders or tissue repair following trauma
XX or burns, in contraceptive regimens, to prevent premature labour, to
XX enhance fetal growth or development, or to treat various cancers
XX including gonadal and adrenal tumours, endometrial and ovarian tumours,
XX and colon cancer.
XX
XX Sequence 120 AA;

```

Query Match 77.0%; Score 67; DB 20; Length 120;  
 Best Local Similarity 100.0%; Pred. No. 0.00024;  
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CASDGLVPRRLQ 13  
 DB 107 casdglvprrlq 119  
 |||||

RESULT 6  
 AAY17870  
 ID AAY17870 standard; Protein; 366 AA.  
 AC AAY17870;

DT 20-AUG-1999 (first entry)

DE Human bone morphogenic protein BMP-17.

KW Human; bone morphogenic protein; BMP-17; BMP-18; cartilage; tendon;  
 KW connective tissue defect; ligament; meniscus; wound healing; growth;  
 KW differentiation; epidermis; muscle; nerve; cardiac muscle.

OS Homo sapiens.

TH Key Location/Qualifiers  
 FT Peptide 1..142  
 FT Protein /label= pro-peptide  
 FT 143..366  
 FT /label= BMP-17

PN W09929718-A2.

PD 17-JUN-1999.

PF 17-NOV-1998; 98WO-US24613.

PR 10-DEC-1997; 97US-0987904.

PA (GEMY ) GENETICS INST INC.

PI Celeste AJ, Murray BL;

DR WPI; 1999-385570/32.

DR N-PSDB; AAX80213.

XX New Purified bone morphogenic protein-17 and -18 (BMP-17 and BMP-18)  
 PT polypeptides, useful for the induction of growth and/or  
 PT differentiation of undifferentiated embryonic and stem cells

PS Claim 16; Page 35-36; 39pp; English.

CC The present sequence is a human bone morphogenic protein designated  
 CC BMP-17. BMP proteins are useful for the induction of growth and/or  
 CC differentiation of undifferentiated embryonic and stem cells, and for  
 CC the treatment of bone, cartilage and other connective tissue defects  
 CC including tendons, ligaments and meniscus, in wound healing and related  
 CC tissue repair, and for treatment of disorders and defects to tissues  
 CC which include epidermis, nerve, muscle, including cardiac muscle, and  
 CC other tissues and wounds, and organs such as liver, lung, epithelium,  
 CC brain, spleen, cardiac, pancreas and kidney tissue. DNA encoding BMP  
 CC proteins can be useful as probes to detect expression of BMP proteins,  
 CC and the vectors containing DNA encoding BMP proteins are useful for  
 CC delivery of the BMP proteins to cells of a patient.

XX Sequence 366 AA;

Query Match 77.0%; Score 67; DB 20; Length 366;  
 Best Local Similarity 100.0%; Pred. No. 0.00078;  
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CASDGLVPRRLQ 13

Db 353 casdglvprrlq 365  
 |||||

RESULT 7  
 AAY17871

ID AAY17871 standard; Protein; 366 AA.

AC AAY17871;

DT 20-AUG-1999 (first entry)

DE Human bone morphogenic protein BMP-18.

KW Human; bone morphogenic protein; BMP-17; BMP-18; cartilage; tendon;  
 KW connective tissue defect; ligament; meniscus; wound healing; growth;  
 KW differentiation; epidermis; muscle; nerve; cardiac muscle.

OS Homo sapiens.

TH Key Location/Qualifiers  
 FT Peptide 1..135  
 FT Protein /label= pro-peptide  
 FT 136..366  
 FT /label= BMP-18

PN W09929718-A2.

PD 17-JUN-1999.

PF 17-NOV-1998; 98WO-US24613.

PR 10-DEC-1997; 97US-0987904.

PA (GEMY ) GENETICS INST INC.

PI Celeste AJ, Murray BL;

DR WPI; 1999-385570/32.

DR N-PSDB; AAX80214.

XX New Purified bone morphogenic protein-17 and -18 (BMP-17 and BMP-18)  
 PT polypeptides, useful for the induction of growth and/or  
 PT differentiation of undifferentiated embryonic and stem cells

PS Claim 20; Page 38-39; 39pp; English.

CC The present sequence is a human bone morphogenic protein designated  
 CC BMP-18. BMP proteins are useful for the induction of growth and/or  
 CC differentiation of undifferentiated embryonic and stem cells, and for  
 CC the treatment of bone, cartilage and other connective tissue defects  
 CC including tendons, ligaments and meniscus, in wound healing and related  
 CC tissue repair, and for treatment of disorders and defects to tissues  
 CC which include epidermis, nerve, muscle, including cardiac muscle, and  
 CC other tissues and wounds, and organs such as liver, lung, epithelium,  
 CC brain, spleen, cardiac, pancreas and kidney tissue. DNA encoding BMP  
 CC proteins can be useful as probes to detect expression of BMP proteins,  
 CC and the vectors containing DNA encoding BMP proteins are useful for  
 CC delivery of the BMP proteins to cells of a patient.

XX Sequence 366 AA;

Query Match 77.0%; Score 67; DB 20; Length 366;  
 Best Local Similarity 100.0%; Pred. No. 0.00078;  
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CASDGLVPRRLQ 13

Db 353 casdglvprrlq 365  
 |||||

RESULT 8

```

AAV13363
ID AAY13363 standard; Protein: 366 AA.
XX
AC AAY13363;
XX
DT 25-JUN-1999 (first entry)
XX
DE Amino acid sequence of protein PRO317.
XX
KW Secreted protein; transmembrane protein; human; enterocolitis;
KW Zollinger-Ellison syndrome; gastrointestinal ulceration;
KW congenital microvillus atrophy; skin disease; cell growth;
KW abnormal keratinocyte differentiation; psoriasis; epithelial cancer;
KW Parkinson's disease; Alzheimer's disease; ALS; neuropathy;
KW fibromodulin; dermal scarring; Usher Syndrome; Atrophla areata;
KW anti-thrombotic; wound healing; tissue repair.
XX
OS Homo sapiens.
XX
PN W09914328-A2.
XX
PD 25-MAR-1999.
XX
PF 16-SEP-1998; 98WO-US19330.
XX
PR 25-NOV-1997; 97US-0066840.
PR 17-SEP-1997; 97US-0059113.
PR 17-SEP-1997; 97US-0059115.
PR 17-SEP-1997; 97US-0059117.
PR 17-SEP-1997; 97US-0059119.
PR 17-SEP-1997; 97US-0059121.
PR 17-SEP-1997; 97US-0059122.
PR 17-SEP-1997; 97US-0059184.
PR 18-SEP-1997; 97US-0059263.
PR 18-SEP-1997; 97US-0059266.
PR 15-OCT-1997; 97US-0062125.
PR 17-OCT-1997; 97US-0062285.
PR 17-OCT-1997; 97US-0062287.
PR 21-OCT-1997; 97US-0063486.
PR 24-OCT-1997; 97US-0062814.
PR 24-OCT-1997; 97US-0062816.
PR 24-OCT-1997; 97US-0063045.
PR 24-OCT-1997; 97US-0063120.
PR 24-OCT-1997; 97US-0063121.
PR 24-OCT-1997; 97US-0063127.
PR 24-OCT-1997; 97US-0063128.
PR 27-OCT-1997; 97US-0063329.
PR 27-OCT-1997; 97US-0063327.
PR 28-OCT-1997; 97US-0063341.
PR 28-OCT-1997; 97US-0063342.
PR 28-OCT-1997; 97US-0063344.
PR 28-OCT-1997; 97US-0063349.
PR 28-OCT-1997; 97US-0063350.
PR 28-OCT-1997; 97US-0063354.
PR 29-OCT-1997; 97US-0063435.
PR 29-OCT-1997; 97US-0063704.
PR 29-OCT-1997; 97US-0063732.
PR 29-OCT-1997; 97US-0063738.
PR 29-OCT-1997; 97US-0063734.
PR 29-OCT-1997; 97US-0064215.
PR 29-OCT-1997; 97US-0063735.
PR 31-OCT-1997; 97US-0063870.
PR 31-OCT-1997; 97US-0064103.
PR 03-NOV-1997; 97US-0064248.
PR 07-NOV-1997; 97US-0064809.
PR 12-NOV-1997; 97US-0065186.
PR 17-NOV-1997; 97US-0065846.
PR 18-NOV-1997; 97US-0065693.
PR 21-NOV-1997; 97US-0066120.
PR 21-NOV-1997; 97US-0066364.
PR 24-NOV-1997; 97US-0066772.
PR 24-NOV-1997; 97US-0066466.
PR 24-NOV-1997; 97US-0066770.

PR 24-NOV-1997; 97US-0066511.
PR 24-NOV-1997; 97US-0066453.
XX
PA (GETH ) GENENTECH INC.
XX
PI Chen J, Goddard A, Gurney AL, Pennica D, Wood WI, Yuan J;
XX
DR WPI; 1999-229533/19.
XX
DR N-PSDB; AAX52234.
XX
PT New isolated human genes and polypeptides used in, e.g. treatment of
PT gastrointestinal ulceration
XX
PS Claim 12; Fig 42; 320pp; English.
XX
CC AAV13344-403 represent secreted and transmembrane human proteins.
CC The cDNA sequences are obtained from cDNA libraries, prepared from
CC fetal lung, fetal kidney, fetal brain, fetal liver and fetal retina.
CC The encoded polypeptides have specific uses based on their homology to
CC known polypeptides, e.g. PRO211 and PRO217 can be used for disorders
CC associated with the preservation and maintenance of gastrointestinal
CC mucosa and the repair of acute and chronic mucosal lesions
CC (e.g. enterocolitis, Zollinger-Ellison syndrome, gastrointestinal
CC ulceration and congenital microvillus atrophy), skin diseases associated
CC with abnormal keratinocyte differentiation (e.g. psoriasis, epithelial
CC cancers such as lung squamous cell carcinoma of the vulva and gliomas),
CC potent effects on cell growth and development, diseases related to
CC growth or survival of nerve cells including Parkinson's disease,
CC Alzheimer's disease, ALS, neuropathies or cancer. PRO265 can be used as
CC for fibromodulin, e.g. for reducing dermal scarring. PRO264 can be used
CC as a target for anti-tumor drugs. PRO533 may be used in the treatment
CC of Usher Syndrome or Atrophla areata; PRO269 can be used as an
CC anti-thrombotic agent; PRO287 polypeptides and portions may have
CC therapeutic applications in wound healing and tissue repair; PRO317 can
CC be used for treating problems of the kidney, uterus, endometrium, blood
CC vessels, or related tissue, e.g. in the heart of genital tract.
XX
SQ Sequence 366 AA;

Query Match 77.0%; Score 67; DB 20; Length 366;
Best Local Similarity 100.0%; Pred. No. 0.00078;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CASDGLVPRRLQ 13
|||||
Db 353 casdglvprlq 365

RESULT 9
AAV03850
ID AAY03850 standard; Protein: 366 AA.
XX
AC AAY03850;
XX
DT 18-JUN-1999 (first entry)
XX
DE Human lefty protein.
XX
KW Nodal protein; lefty protein; TGF-beta; sexual development; human;
KW pituitary; cartilage; osteoarthritis; osteoporosis; haematopoiesis;
KW periodontal disease; wound healing; tissue repair; tumour; cancer;
KW interstitial lung disease; autoimmunity; leukaemia; lymphoma; immunity;
KW immunosuppression; inflammatory bowel disease; myelosuppression;
KW infectious disease; bone.
XX
OS Homo sapiens.
XX
PH Key Location/Qualifiers
FT Peptide 1..18 /note= "signal peptide"
FT Protein 19..366 /note= "mature protein"

```

FT Domain 78..364  
 FT /note- "first predicted TGF-beta like domain of lefty"  
 FT 136..366  
 FT Domain /note- "second predicted TGF-beta like domain of lefty"  
 FT 143..366  
 FT /note- "third predicted TGF-beta like domain of lefty"  
 XX  
 PN W09509198-A1.  
 XX  
 PD 25-FEB-1999.  
 XX  
 XX 20-AUG-1998; 98WO-US17211.  
 PF  
 XX 21-AUG-1997; 97US-0056565.  
 PR  
 XX (HUMA-) HUMAN GENOME SCI INC.  
 PA  
 XX Ebner R, Ruben SM, Soppet DR;  
 PI  
 DR WPI: 1999-190173/16.  
 DR N-PSDB; AAX31925.  
 XX  
 XX New isolate human Nodal and Lefty polypeptides  
 XX  
 PS Claim 1: Fig 1B; 182pp; English.  
 XX  
 CC The present invention relates to novel human nodal and lefty proteins  
 CC which are members of the TGF-beta family. The human nodal and lefty  
 CC proteins may be involved in a developmental process such as the correct  
 CC formation of various structures or in one or more post-developmental  
 CC capacities including sexual development, pituitary hormone production,  
 CC and the creation of bone and cartilage. The Nodal and Lefty polypeptides  
 CC are useful for enhancing or enriching the growth and/or differentiation  
 CC of specific cell populations, eg. embryonic cells or stem cells. They can  
 CC be used to treat such conditions as osteoarthritis, osteoporosis, and  
 CC other abnormalities of bone, cartilage, muscle, tendon, ligament, and/or  
 CC other connective tissues and/or organs such as liver, lung, cardiac,  
 CC pancreas, and kidney. Compositions containing nodal and lefty proteins  
 CC may be useful for growth formation, for treating periodontal disease and  
 CC for modulating haematopoiesis, wound healing and tissue repair. They can  
 CC also be used for the treatment of tumours, cancers, interstitial lung  
 CC disease, and any dysregulation of the growth and differentiation patterns  
 CC of cell function including autoimmunity, arthritis, leukaemia, lymphomas,  
 CC immunosuppression, immunity, humoral immunity, inflammatory bowel  
 CC disease, myelosuppression, or infectious diseases. The present sequence  
 CC represents a human lefty polypeptide. The cDNA encoding the lefty  
 CC protein is deposited under the ATCC deposit No. 209091.  
 XX  
 SQ Sequence 366 AA;  
 Query Match 77.0%; Score 67; DB 20; Length 366;  
 Best Local Similarity 100.0%; Pred. No. 0.00078;  
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 CASDQALVPRRLQ 13  
 Db 353 casdgalvprrlq 365  
 RESULT 10  
 ID AAY05287  
 AC AAY05287 standard; Protein; 366 AA.  
 XX  
 XX AAY05287;  
 DT 22-JUN-1999 (first entry)  
 XX  
 DE EGF-like homologue EBAF-2.  
 XX  
 XX Antibody; PRO187; PRO533; PRO214; PRO240; PRO211; PRO230; PRO261; PRO246;  
 KW EBAF-2; inhibitor; tumour growth; cancer; EGF-like homologue;  
 KW FGF-8 homologue.  
 XX

XX Homo sapiens.  
 OS  
 XX W09914327-A2.  
 PN  
 XX 25-MAR-1999.  
 PD  
 XX 10-SEP-1998; 98WO-US18824.  
 PF  
 XX 25-NOV-1997; 97US-0066840.  
 PR  
 PR 17-SEP-1997; 97US-0059114.  
 PR 17-SEP-1997; 97US-0059117.  
 PR 18-SEP-1997; 97US-0059263.  
 PR 15-OCT-1997; 97US-0062125.  
 PR 17-OCT-1997; 97US-0062285.  
 PR 17-OCT-1997; 97US-0062287.  
 PR 24-OCT-1997; 97US-0062816.  
 PR 29-OCT-1997; 97US-0063704.  
 XX  
 XX (GETH ) GENENTECH INC.  
 PA  
 XX Botstein D, Goddard A, Gurney A, Hillan K, Lawrence DA;  
 PI Roy M, Wood WI;  
 PI  
 XX WPI: 1999-229532/19.  
 DR N-PSDB; AAX28437.  
 DR  
 XX Antibodies against specific proteins overexpressed in tumours  
 PT  
 XX Example 1: Fig 30; 130pp; English.  
 PS  
 CC This sequence represents the EGF-like homologue EBAF-2.  
 CC The invention relates to antibodies (Ab) that bind to any of the  
 CC polypeptides (I) designated PRO187; PRO533; PRO214; PRO240; PRO211;  
 CC PRO230; PRO261; PRO246 or EBAF-2. The Ab, or other agents that inhibit  
 CC expression and/or activity of (I) are used: (i) to inhibit growth of  
 CC tumours; and (ii) as diagnostic/prognostic reagents for detection or  
 CC quantification of (I) in cells or tissues, by standard immunoassays, with  
 CC overexpression being indicative of cancer. For therapeutic use, the Ab  
 CC may be conjugated to a toxin, chemotherapeutic agent or radioisotope.  
 CC Genes expressing (I), many of which are growth factor homologues, are  
 CC overexpressed in some cases of cancer.  
 XX  
 SQ Sequence 366 AA;  
 Query Match 77.0%; Score 67; DB 20; Length 366;  
 Best Local Similarity 100.0%; Pred. No. 0.00078;  
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 CASDQALVPRRLQ 13  
 Db 353 casdgalvprrlq 365  
 RESULT 11  
 ID AAY88575  
 AC AAY88575 standard; Protein; 366 AA.  
 XX  
 XX AAY88575;  
 DT 09-AUG-2000 (first entry)  
 XX  
 DE Human PRO317 amino acid sequence.  
 XX  
 XX Antibody; PRO187; PRO533; PRO214; PRO240; PRO211; PRO230; PRO261; PRO246;  
 KW PRO317; tumour growth inhibitor; cancer; diagnosis; treatment; human;  
 KW cell growth; proliferation; transforming growth factor; ADEPT;  
 KW antibody dependent enzyme mediated prodrug therapy.  
 XX  
 OS Homo sapiens.  
 XX  
 PN W0200015666-A2.

XX PD 23-MAR-2000.  
 XX PF 08-SEP-1999; 99WO-US20594.  
 XX PR 10-SEP-1998; 98US-0099803.  
 XX PR 10-SEP-1998; 98WO-US18824.  
 XX PA (GETH ) GENENTECH INC.  
 XX PI Goddard A, Gurney AL, Hillan KJ, Roy MA, Wood WI, Botstein D;  
 XX WPI; 2000-271386/23.  
 XX DR N-PSDB; AAA30056.  
 XX New isolated antibodies which bind to specific polypeptides used for  
 diagnosis and treatment of neoplastic cell growth and proliferation -  
 Example 9; Fig 18; 200pp; English.  
 XX This sequence represents a human PRO317 amino acid sequence. PRO317  
 shares sequence homology with members of the transforming growth factor  
 beta superfamily of proteins. The invention relates to isolated  
 antibodies which bind to a polypeptide. The "PRO" polypeptides are  
 encoded by genes which are over expressed in the genome of tumour cells.  
 Vectors and host cells comprising the nucleic acid encoding the  
 antibodies are used in the production of the antibodies. The antibodies  
 and nucleic acids encoding them are used for diagnosing a tumour in a  
 mammal. The antibodies are used for inhibiting the growth of tumour cells  
 and identifying compounds that inhibit a biological or immunological  
 activity of and/or expression of a PRO187, PRO533, PRO214, PRO240,  
 PRO211, PRO230, PRO261, PRO246 or PRO317 polypeptide. The antibody can be  
 used in antibody dependent enzyme mediated prodrug therapy (ADEPT) by  
 conjugating the antibody to a prodrug-activating enzyme which converts a  
 prodrug to an anti-cancer drug. The antibodies can be fluorescently  
 labelled and monitored by light microscopy, flow cytometry or fluorimetry  
 for diagnosis and prognosis of tumours.  
 XX Sequence 366 AA;  
 SQ

Query Match 77.0%; Score 67; DB 21; Length 366;  
 Best Local Similarity 100.0%; Pred. No. 0.00078;  
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CASDGLVPRRLQ 13  
 |||||  
 Db 353 casdglvprrlq 365

RESULT 12  
 AAB95157  
 ID AAB95157 standard; Protein; 366 AA.  
 AC AAB95157;  
 XX

DT 26-JUN-2001 (first entry)  
 XX

DE Human protein sequence SEQ ID NO:17194.  
 XX

KW Human; primer; detection; diagnosis; antisense therapy; gene therapy.  
 XX

OS Homo sapiens.  
 XX

PN EP1074617-A2.  
 XX

XX EP1074617-A2.  
 XX

PD 07-FEB-2001.  
 XX

XX 28-JUL-2000; 2000EP-0116126.  
 PF

XX 29-JUL-1999; 99JP-0248036.  
 PR

XX 27-AUG-1999; 99JP-0300253.  
 PR

XX 11-JAN-2000; 2000JP-0118776.  
 PR

PR 02-MAY-2000; 2000JP-0183767.  
 XX 09-JUN-2000; 2000JP-0241899.  
 XX (HELI-) HELIX RES INST.  
 XX Ota T, Isogai T, Nishikawa T, Hayashi K, Saito K, Yamamoto J;  
 PI Ishii S, Sugiyama T, Wakamatsu A, Nagai K, Otsuki T;  
 XX WPI; 2001-318749/34.  
 XX Primer sets for synthesizing polynucleotides, particularly the 5602  
 full-length cDNAs defined in the specification, and for the detection  
 and/or diagnosis of the abnormality of the proteins encoded by the  
 full-length cDNAs -

PS Claim 8; SEQ ID 17194; 2537pp + CD ROM; English.

XX The present invention describes primer sets for synthesising 5602  
 full-length cDNAs defined in the specification. Where a primer set  
 comprises: (a) an oligo-dT primer and an oligonucleotide complementary  
 to the complementary strand of a polynucleotide which comprises one of  
 the 5602 nucleotide sequences defined in the specification, where the  
 oligonucleotide comprises at least 15 nucleotides; or (b) a combination  
 of an oligonucleotide comprising a sequence complementary to the  
 complementary strand of a polynucleotide which comprises a 5'-end  
 sequence and an oligonucleotide comprising a sequence complementary to a  
 polynucleotide which comprises a 3'-end sequence, where the  
 oligonucleotide comprises at least 15 nucleotides and the combination of  
 the 5'-end sequence/3'-end sequence is selected from those defined in  
 the specification. The primer sets can be used in antisense therapy and  
 in gene therapy. The primers are useful for synthesising polynucleotides,  
 particularly full-length cDNAs. The primers are also useful for the  
 detection and/or diagnosis of the abnormality of the proteins encoded by  
 the full-length cDNAs. The primers allow obtaining of the full-length  
 cDNAs easily without any specialised methods. AAH03166 to AAH13628 and  
 AAH13633 to AAH18742 represent human cDNA sequences; AAB92446 to  
 AAB95893 represent human amino acid sequences; and AAH13629 to AAH13632  
 represent oligonucleotides, all of which are used in the exemplification  
 of the present invention.

SQ Sequence 366 AA;

Query Match 77.0%; Score 67; DB 22; Length 366;  
 Best Local Similarity 100.0%; Pred. No. 0.00078;  
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CASDGLVPRRLQ 13  
 |||||  
 Db 353 casdglvprrlq 365

RESULT 13  
 AAB68600  
 ID AAB68600 standard; Protein; 366 AA.  
 XX

AC AAB68600;  
 XX

DT 27-APR-2001 (first entry)  
 XX

DE PRO317.  
 XX

XX Cytostatic; PRO protein; tumour; cancer.  
 KW

OS Homo sapiens.  
 XX

XX WO200105836-A1.  
 PN

XX 25-JAN-2001.  
 PD

XX 20-DEC-1999; 99WO-US30999.  
 PF

XX 20-JUL-1999; 99US-0144758.  
 PR

```

PR 26-JUL-1999; 99US-0145698.
PR 08-SEP-1999; 99WO-US20594.
PR 13-SEP-1999; 99WO-US20944.
PR 15-SEP-1999; 99WO-US21090.
PR 05-OCT-1999; 99WO-US23089.
PR 29-NOV-1999; 99WO-US28214.
PR 30-NOV-1999; 99WO-US28313.
PR 16-DEC-1999; 99WO-US30095.
PR 20-DEC-1999; 99WO-US30911.
PR 02-DEC-1999; 99WO-US28564.
XX (GETH ) GENENTECH INC.
PA
XX
XX Botstein D, Goddard A, Gurney AL, Hillan KJ, Roy MA, Wood WI;
PI WPI; 2001-091968/10.
DR N-PSDB; AAF60376.
XX
XX New antibody that binds to a PRO polypeptide, e.g. PRO187 and PRO533,
PT useful for diagnosing and treating cancers -
PT
XX Claim 61; Fig 18; 196pp; English.
PS
XX The present invention relates to PRO proteins and coding sequences. The
CC present sequence is one such PRO protein. It was found that the PRO genes
CC are amplified in the genome of tumour cells. The gene amplification is
CC expected to be associated with the overexpression of the gene product and
CC contributes to tumourigenesis. Therefore, antagonists of PRO proteins are
CC useful for the treatment of benign or malignant tumours, leukaemias,
CC lymphoid malignancies and other disorders such as neuronal, glial,
CC astrocytal, hypothalamic, glandular, epithelial, inflammatory and
CC immunologic disorders.
XX
XX Sequence 366 AA;
SQ
Query Match 77.0%; Score 67; DB 22; Length 366;
Best Local Similarity 100.0%; Pred. No. 0.00078;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 CASD GALVPRRLQ 13
DB 353 casdgalvprrlq 365
RESULT 14
AAB80231
ID AAB80231 standard; Protein; 366 AA.
AC AAB80231;
XX
XX 24-APR-2001 (first entry)
XX
XX Human PRO317 protein.
XX
XX Human; PRO; dermatologic; antipsoriatic; cytostatic; antiinflammatory;
KW antiparkinsonian nootropic; neuroprotective; vulnery; cardiant;
KW antiangiogenic; vasotropic; antiasthmatic; antirheumatic; cancer;
KW antithalritic; antinfertility; antidiabetic; antiviral; diabetes;
KW ophthalmologic; gene therapy; skin disease; gastrointestinal disorder;
KW ischaemia; inflammation.
XX
XX Homo sapiens.
XX
XX WO200104311-A1.
XX
XX 18-JAN-2001.
XX
XX 22-FEB-2000; 2000WO-US04414.
XX
XX 07-JUL-1999; 99US-0143048.
XX 26-JUL-1999; 99US-0145698.
XX 28-JUL-1999; 99US-0146222.
XX 08-SEP-1999; 99WO-US20594.
XX 13-SEP-1999; 99WO-US20944.

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PR 15-SEP-1999; 99WO-US21090.
PR 15-SEP-1999; 99WO-US21547.
PR 05-OCT-1999; 99WO-US23089.
PR 29-NOV-1999; 99WO-US28214.
PR 30-NOV-1999; 99WO-US28313.
PR 16-DEC-1999; 99WO-US30095.
PR 20-DEC-1999; 99WO-US30911.
PR 20-DEC-1999; 99WO-US30999.
PR 05-JAN-2000; 99WO-US00219.
XX (GETH ) GENENTECH INC.
PA
XX
XX Ashkenazi AJ, Botstein D, Desnoyers L, Eaton DL, Ferrara N;
PI Filvaroff E, Fong S, Gao W, Gerber H, Gerritsen ME, Goddard A;
PI Godowski PJ, Grimaldi CJ, Gurney AL, Hillan KJ, Kljavin IJ;
PI Mather JP, Pan J, Paoni NF, Roy MA, Stewart TA, Tumas D;
PI Williams PM, Wood WI;
XX WPI; 2001-081051/09.
DR N-PSDB; AAF72392.
XX
XX Sixty one nucleic acids encoding PRO polypeptides which are useful in
PT the treatment of skin diseases (e.g. psoriasis), cancers (e.g. lung
PT squamous cell carcinoma) and neurodegenerative diseases (e.g.
PT Alzheimer's disease) -
XX
XX Claim 1; Fig 42; 393pp; English.
PS
XX The present sequence is one of sixty one novel secreted and
CC transmembrane PRO polypeptides. The PRO polypeptides are
CC useful for treating skin diseases (e.g. psoriasis), cancers (e.g. lung
CC squamous cell carcinoma), gastrointestinal disorders (e.g.
CC enterocolitis), neurodegenerative diseases (e.g. Alzheimer's disease,
CC Parkinson's disease), wound repair, cardiovascular disorders (e.g.
CC endometrial bleeding angiogenesis, ischaemias such as coronary
CC ischaemia, atherosclerosis), inflammatory disorders (e.g. asthma,
CC rheumatoid arthritis, multiple sclerosis), infertility, AIDS and
CC diabetes and retinal disorders such as retinitis pigmentosum.
CC The PRO nucleic acids have applications in molecular biology, including
CC use as hybridization probes, and in chromosome and gene mapping.
XX
XX Sequence 366 AA;
SQ
Query Match 77.0%; Score 67; DB 22; Length 366;
Best Local Similarity 100.0%; Pred. No. 0.00078;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 CASD GALVPRRLQ 13
DB 353 casdgalvprrlq 365
RESULT 15
AAB19837
ID AAB19837 standard; Protein; 366 AA.
XX
XX AAB19837;
XX
XX 05-MAR-2001 (first entry)
XX
XX Endometrial bleeding associated factor (ebaf) protein.
XX
XX Endometrial bleeding associated factor; ebaf; human;
KW chromosome 1q42.1; neurodegenerative disease; Alzheimer's disease;
KW Parkinson's disease; Huntington's chorea; dementia;
KW amyotrophic lateral sclerosis; Pick's disease; therapy.
XX
XX Homo sapiens.
XX
XX WO200006068-A2.
XX
XX 09-NOV-2000.

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XX 28-APR-2000; 2000WO-US11623.
XX
XX 29-APR-1999; 99US-0302094.
XX
XX (NSHO-) NORTH SHORE-LONG ISLAND JEWISH RES.
XX
XX Tabibzadeh S;
XX
XX WPI; 2001-040876/05.
XX
XX N-PSDB; AAA88913.
XX
XX Inducing growth and enhancing survival of nervous tissue by contacting
XX with endometrial bleeding associated factor protein
XX
XX Disclosure; Fig 2; 23pp; English.
XX
XX The present sequence is that of human endometrial bleeding
XX associated factor (ebaf). A claimed method for inducing growth
XX and enhancing survival of nervous tissue comprises contacting the
XX tissue with ebaf or a nucleic acid encoding ebaf in vitro or in
XX vivo. The method can be used to treat damaged or degenerated
XX nervous tissue resulting from injury associated with trauma,
XX diabetes, kidney dysfunction, ischaemia or use of therapeutic
XX agents, or to treat a neurodegenerative disease such as Alzheimer's
XX disease, Parkinson's disease, Huntington's chorea, amyotrophic
XX lateral sclerosis, dementia, or Pick's disease (all claimed).
XX
SQ Sequence 366 AA;

Query Match          77.0%; Score 67; DB 22; Length 366;
Best Local Similarity 100.0%; Pred. No. 0.00078;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CASDGLVPRRLQ 13
   | | | | | | | | | |
Db 353 casdgalvprlq 365

```

Search completed: September 10, 2002, 10:45:12  
Job time: 265 sec

GenCore version 4.5  
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OM protein - protein search, using sw model

Run on: September 10, 2002, 10:44:22 ; Search time 25.08 Seconds  
(without alignments)  
110.364 Million cell updates/sec

Title: us-09-674-254-3

Perfect score: 87  
Sequence: 1 CASDGLVPRRLQHRP 16

Scoring table:  
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Gapop 10.0 , Gapext 0.5

Searched: 562222 seqs, 172994929 residues

Total number of hits satisfying chosen parameters: 562222

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPTREMBL\_19:\*  
1: sp\_archaea:\*  
2: sp\_bacteria:\*  
3: sp\_fungi:\*  
4: sp\_human:\*  
5: sp\_invertebrate:\*  
6: sp\_mammal:\*  
7: sp\_mhc:\*  
8: sp\_organellie:\*  
9: sp\_phage:\*  
10: sp\_plant:\*  
11: sp\_rodent:\*  
12: sp\_virus:\*  
13: sp\_vertebrate:\*  
14: sp\_unclassified:\*  
15: sp\_rvirus:\*  
16: sp\_bacteriap:\*  
17: sp\_archeap:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	44	50.6	67	4 Q9UHN8	Q9uhn8 homo sapien
2	44	50.6	99	4 Q9UI41	Q9ui41 homo sapien
3	44	50.6	120	4 Q9UHW7	Q9uhm7 prunus necr
4	44	50.6	152	4 Q9UBR5	Q9ubr5 homo sapien
5	44	50.6	219	12 Q71131	Q71131 prunus necr
6	44	50.6	224	12 Q9YKE6	Q9yke6 prunus necr
7	44	50.6	224	12 Q9YKE3	Q9yke3 prunus necr
8	44	50.6	224	12 Q70915	Q70915 prunus necr
9	44	50.6	224	12 Q70917	Q70917 prunus necr
10	44	50.6	224	12 Q9IMR7	Q9imr7 prunus necr
11	44	50.6	224	12 Q9IMR5	Q9imr5 prunus necr
12	44	50.6	224	12 Q9IMR2	Q9imr2 prunus necr
13	44	50.6	224	12 Q9IMQ9	Q9imq9 prunus necr
14	44	50.6	224	12 Q9IMQ7	Q9imq7 prunus necr
15	44	50.6	224	12 Q9IMQ3	Q9imq3 prunus necr
16	44	50.6	224	12 Q9IMQ1	Q9imq1 prunus necr

17	44	50.6	224	12 Q99AV0	Q99av0 prunus necr
18	44	50.6	224	12 Q991T8	Q991t8 prunus necr
19	44	50.6	224	12 Q99AU8	Q99au8 prunus necr
20	44	50.6	224	12 Q9YKF2	Q9ykf2 prunus necr
21	44	50.6	224	12 Q9YKF1	Q9ykf1 prunus necr
22	44	50.6	224	12 Q9YKE9	Q9yke9 prunus necr
23	44	50.6	224	12 Q9YKE8	Q9yke8 prunus necr
24	44	50.6	224	12 Q9YKE2	Q9yke2 prunus necr
25	44	50.6	224	12 Q9YKD9	Q9ykd9 prunus necr
26	44	50.6	224	12 Q86920	Q86920 prunus necr
27	44	50.6	224	12 Q9ICE6	Q9ice6 prunus necr
28	44	50.6	224	12 Q91H48	Q91h48 prunus necr
29	44	50.6	224	12 Q91H47	Q91h47 prunus necr
30	44	50.6	224	12 Q91H46	Q91h46 prunus necr
31	44	50.6	522	16 Q9JZE2	Q9jze2 neisseria m
32	44	50.6	522	16 Q9JUH1	Q9juh1 neisseria m
33	43	49.4	151	4 Q9H4T7	Q9h4t7 homo sapien
34	43	49.4	865	5 Q9N998	Q9n998 leishmania
35	42.5	48.9	656	3 Q01408	Q01408 neurospora
36	41.5	47.7	327	16 Q49822	Q49822 mycobacteri
37	41	47.1	313	16 Q98MP6	Q98mp6 rhizobium l
38	41	47.1	606	16 Q92CQ1	Q92cq1 listeria in
39	41	47.1	871	4 Q9Y5C3	Q9y5c3 homo sapien
40	41	47.1	938	4 Q9Y5F7	Q9y5f7 homo sapien
41	41	47.1	941	11 Q91XX0	Q91xx0 mus musculu
42	40	46.0	106	10 P93601	P93601 triticum ae
43	40	46.0	109	2 Q939U2	Q939u2 rhodovulum
44	40	46.0	123	16 Q98EC6	Q98ec6 rhizobium l
45	40	46.0	168	2 Q9XDC3	Q9xdc3 herbaspirill

## ALIGNMENTS

RESULT 1  
ID Q9UHN8 PRELIMINARY; PRT; 67 AA.  
AC Q9UHN8;  
DT 01-MAY-2000 (Tremblrel. 13, Created)  
DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)  
DT 01-DEC-2001 (Tremblrel. 19, Last annotation update)  
DE CHEMOKINE-LIKE FACTOR 3.  
GN CKLF3.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Han W.L.;  
RL Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.  
DR EMBL: AF135381; AAF19600.1;  
SQ SEQUENCE 67 AA; 7652 MW; 7BEB754D8880F1F9 CRC64;

Query Match 50.6%; Score 44; DB 4; Length 67;  
Best Local Similarity 50.0%; Pred. No. 2.1;  
Matches 8; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

QY 1 CASDGLVPRRLQHRP 16  
| :|||: | :|  
Db 36 CLADGALIVRKLLFNP 51

RESULT 2  
ID Q9UI41 PRELIMINARY; PRT; 99 AA.  
AC Q9UI41;  
DT 01-MAY-2000 (Tremblrel. 13, Created)  
DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)  
DT 01-DEC-2001 (Tremblrel. 19, Last annotation update)  
DE CHEMOKINE-LIKE FACTOR 1.  
GN CKLF1.



```

OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21308461; PubMed=11415443;
RA Han W., Lou Y., Tang J., Zhang Y., Chen Y., Li Y., Gu W., Huang J.,
RA Han W., Tang Y., Li F., Song Q., Di C., Wang L., Shi Q., Sun R.,
RA Xia D., Rui M., Tang J., Ma D.;
RT "Molecular cloning and characterization of chemokine-like factor 1
RT (CKLF1), a novel human cytokine with unique structure and potential
RT chemotactic activity.";
RL Biochem. J. 357:127-135(2001).
DR EMBL; AF096895; AAF06722.1; -.
SQ SEQUENCE 99 AA; 10923 MW; 1F5EBF5AA7A9479E CRC64;

Query Match 50.6%; Score 44; DB 4; Length 99;
Best Local Similarity 50.0%; Pred. No. 3.1;
Matches 8; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

QY 1 CASD GALVPRRLOHRP 16
I :||||: |:-|
DB 68 CLADGALIVKLLFNP 83

RESULT 3
Q9UHM7 PRELIMINARY; PRT; 120 AA.
AC Q9UHM7;
DT 01-MAY-2000 (TReMBLrel. 13, Created)
DT 01-MAY-2000 (TReMBLrel. 13, Last sequence update)
DT 01-DEC-2001 (TReMBLrel. 19, Last annotation update)
DE CHEMOKINE-LIKE FACTOR 4.
GN CKLF4.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Han W.L.;
RL Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF145216; AAF19350.1; -.
SQ SEQUENCE 120 AA; 13899 MW; BF0C011077F24C13 CRC64;

Query Match 50.6%; Score 44; DB 4; Length 120;
Best Local Similarity 50.0%; Pred. No. 3.7;
Matches 8; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

QY 1 CASD GALVPRRLOHRP 16
I :||||: |:-|
DB 89 CLADGALIVKLLFNP 104

RESULT 4
Q9UBR5 PRELIMINARY; PRT; 152 AA.
AC Q9UBR5;
DT 01-MAY-2000 (TReMBLrel. 13, Created)
DT 01-MAY-2000 (TReMBLrel. 13, Last sequence update)
DT 01-JUN-2001 (TReMBLrel. 17, Last annotation update)
DE TRANSMEMBRANE PROTEOLIPID (HSPC224) (UNKNOWN) (PROTEIN FOR
DE MGC:10558).
GN C32 OR CKLF2.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.

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RC TISSUE=PANCREAS;
RA Zhang J.S., Nelson M., Wang L., Smith D.I.;
RL Submitted (APR-1998) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RA Han W., Gu W., Li Y., Zhang Y., Song Q., Di C., Ma D.;
RL Submitted (MAR-1999) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RC TISSUE=UMBILICAL CORD BLOOD;
RA Ye M., Zhang Q.H., Zhou J., Shen Y., Wu X.Y., Guan Z.Q., Wang L.,
RA Fan H.Y., Mao Y.F., Dai M., Huang Q.H., Chen S.J., Chen Z.;
RT "Human full length cDNA cloned from cd34+ stem cells.";
RL Submitted (MAY-1999) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE FROM N.A.
RC TISSUE=PANCREATIC ADENOCARCINOMA;
RA Strausberg R.;
RL Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF057306; AAF21255.1; -.
DR EMBL; AF135380; AAF19599.1; -.
DR EMBL; AF151058; AAF36144.1; -.
DR EMBL; BC004380; AAH04380.1; -.
KW Transmembrane.
SQ SEQUENCE 152 AA; 17170 MW; 6149D6D2B6AED9F3 CRC64;

Query Match 50.6%; Score 44; DB 4; Length 152;
Best Local Similarity 50.0%; Pred. No. 4.7;
Matches 8; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

QY 1 CASD GALVPRRLOHRP 16
I :||||: |:-|
DB 121 CLADGALIVKLLFNP 136

RESULT 5
O71131 PRELIMINARY; PRT; 219 AA.
ID O71131;
AC O71131;
DT 01-AUG-1998 (TReMBLrel. 07, Created)
DT 01-AUG-1998 (TReMBLrel. 07, Last sequence update)
DT 01-DEC-2001 (TReMBLrel. 19, Last annotation update)
DE COAT PROTEIN (FRAGMENT).
OS Prunus necrotic ringspot virus.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Bromoviridae;
OC Ilarvirus.
OX NCBI_TaxID=37733;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CH61;
RX MEDLINE=98343741; PubMed=9680147;
RA Hammond R.W., Crosslin J.M.;
RT "Virulence and molecular polymorphism of Prunus necrotic ringspot
RT virus isolates.";
RL J. Gen. Virol. 79:1815-1823(1998).
DR EMBL; AF034989; AAC41025.1; -.
DR InterPro; IPR002681; Ilar_coat.
DR Pfam; PF01787; Ilar_coat; 1.
FT NON_TER 219
FT SEQUENCE 219 AA; 24491 MW; 0B2748B65C5DE4D5 CRC64;

Query Match 50.6%; Score 44; DB 12; Length 219;
Best Local Similarity 60.0%; Pred. No. 6.8;
Matches 9; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

QY 1 CASD GALVPRRLOHR 15
I :||||: |:-|
DB 20 CHPN GALVPLRAQOR 34

RESULT 6

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DR	EMBL; AJ133208; CAB37310.1; -;
DR	EMBL; AF170160; AAF89709.1; -;
DR	InterPro; IPR002681; Ilar_coat.
DR	Pfam; PF01787; Ilar_coat; 1.
KW	Coat protein.
SQ	SEQUENCE 224 AA; 24927 MW; E215BCEEDIC0703F CRC64;
Query Match 50.6%; Score 44; DB 12; Length 224;	
Best Local Similarity 60.0%; Pred. No. 7;	
Matches 9; Conservative 1; Mismatches 5; Indels 0; Gap	
Qy	1 CASDGLVPRRLQHR 15 I :
Dd	20 CHPNGALVPLRAOQR 34
RESULT 8	
O70915	PRELIMINARY; PRT; 224 AA.
ID O70915	
AC O70915	
DT 01-AUG-1998 (TrEMBLrel. 07, Created)	
DT 01-AUG-1998 (TrEMBLrel. 07, Last sequence update)	
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)	
DE COAT PROTEIN.	
GN 3B.	
OS Prunus necrotic ringspot virus.	
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Bromoviridae.	
OC Ilaryvirus.	
OX NCBI_TaxID=37733;	
RN [1]	
RP SEQUENCE FROM N.A.	
RC STRAIN=MISSION;	
RA Scott S.W., Zimmerman M.T., Ge X., Mackenzie D.J.;	
RT "The coat proteins and putative movement proteins of isolates of	
RT Prunus necrotic ringspot virus from different host species and	
RT geographic origins are extensively conserved.";	
FL Eur. J. Plant Pathol. 104:155-161(1998).	
DR EMBL; AF013285; AAC16499.1; -;	
DR InterPro; IPR002681; Ilar_coat.	
DR Pfam; PF01787; Ilar_coat; 1.	
SQ SEQUENCE 224 AA; 25088 MW; CA6FB9979E4FCA87 CRC64;	
Query Match 50.6%; Score 44; DB 12; Length 224;	
Best Local Similarity 60.0%; Pred. No. 7;	
Matches 9; Conservative 1; Mismatches 5; Indels 0; Gap	
Qy	1 CASDGLVPRRLQHR 15 I :
Dd	20 CHPNGALVPLRAOQR 34
RESULT 9	
O70917	PRELIMINARY; PRT; 224 AA.
ID O70917	
AC O70917	
DT 01-AUG-1998 (TrEMBLrel. 07, Created)	
DT 01-AUG-1998 (TrEMBLrel. 07, Last sequence update)	
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)	
DE COAT PROTEIN.	
GN 3B.	
OS Prunus necrotic ringspot virus.	
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Bromoviridae.	
OC Ilaryvirus.	
OX NCBI_TaxID=37733;	
RN [1]	
RP SEQUENCE FROM N.A.	
RC STRAIN=PRUNE;	
RA Scott S.W., Zimmerman M.T., Ge X., Mackenzie D.J.;	
RT "The coat proteins and putative movement proteins of isolates of	
RT Prunus necrotic ringspot virus from different host species and	
RT geographic origins are extensively conserved.";	

RL Eur. J. Plant Pathol. 104:155-161(1998).  
DR EMBL: AF013286; AAC16501.1; -.  
DR InterPro: IPR002681; Iilar\_coat.  
DR Pfam: PF01787; Iilar\_coat; 1.  
SQ SEQUENCE 224 AA; 24939 MW; 8D03DAAEDC21BACF CRC64;

Query Match 50.6%; Score 44; DB 12; Length 224;  
Best Local Similarity 60.0%; Pred. No. 7;  
Matches 9; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

QY 1 CASD GALVPRRLQHR 15  
| :||||| | | |  
Db 20 CHPNGALVPLRAQQR 34

## RESULT 10

Q9IMR7 ID Q9IMR7 PRELIMINARY; PRT; 224 AA.  
AC Q9IMR7;  
DT 01-OCT-2000 (TrEMBLrel. 15, Created)  
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)  
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)  
DE CAPSID PROTEIN.  
GN CP.  
OS Prunus necrotic ringspot virus.  
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Bromoviridae;  
OC Iilarvirus.  
OX NCBI\_TaxID=37733;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN-PS 7/11;  
RX MEDLINE=20349238; PubMed=10893149;  
RA Vaskova D., Petrzik K., Karesova R.;  
RT "Variability and molecular typing of the woody-tree infecting prunus  
RT necrotic ringspot Iilarvirus.";  
RL Arch. Virol. 145:699-709(2000).  
DR EMBL: AF170161; AAF89711.1; -.  
DR InterPro: IPR002681; Iilar\_coat.  
DR Pfam: PF01787; Iilar\_coat; 1.  
SQ SEQUENCE 224 AA; 24965 MW; 9D1EB6CBC04DDFDA CRC64;

Query Match 50.6%; Score 44; DB 12; Length 224;  
Best Local Similarity 60.0%; Pred. No. 7;  
Matches 9; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

QY 1 CASD GALVPRRLQHR 15  
| :||||| | | |  
Db 20 CHPNGALVPLRAQQR 34

## RESULT 11

JIMR5 ID Q9IMR5 PRELIMINARY; PRT; 224 AA.  
AC Q9IMR5;  
DT 01-OCT-2000 (TrEMBLrel. 15, Created)  
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)  
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)  
DE CAPSID PROTEIN.  
GN CP.  
OS Prunus necrotic ringspot virus.  
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Bromoviridae;  
OC Iilarvirus.  
OX NCBI\_TaxID=37733;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN-PS 7/12;  
RX MEDLINE=20349238; PubMed=10893149;  
RA Vaskova D., Petrzik K., Karesova R.;  
RT "Variability and molecular typing of the woody-tree infecting prunus  
RT necrotic ringspot Iilarvirus.";  
RL Arch. Virol. 145:699-709(2000).

DR EMBL: AF170162; AAF89713.1; -.  
DR InterPro: IPR002681; Iilar\_coat.  
DR Pfam: PF01787; Iilar\_coat; 1.  
SQ SEQUENCE 224 AA; 24906 MW; F12975BF70C89ED CRC64;

Query Match 50.6%; Score 44; DB 12; Length 224;  
Best Local Similarity 60.0%; Pred. No. 7;  
Matches 9; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

QY 1 CASD GALVPRRLQHR 15  
| :||||| | | |  
Db 20 CYPNGALVPLRAQQR 34

## RESULT 12

Q9IMR2 ID Q9IMR2 PRELIMINARY; PRT; 224 AA.  
AC Q9IMR2;  
DT 01-OCT-2000 (TrEMBLrel. 15, Created)  
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)  
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)  
DE CAPSID PROTEIN.  
GN CP.  
OS Prunus necrotic ringspot virus.  
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Bromoviridae;  
OC Iilarvirus.  
OX NCBI\_TaxID=37733;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN-7/20;  
RX MEDLINE=20349238; PubMed=10893149;  
RA Vaskova D., Petrzik K., Karesova R.;  
RT "Variability and molecular typing of the woody-tree infecting prunus  
RT necrotic ringspot Iilarvirus.";  
RL Arch. Virol. 145:699-709(2000).  
DR EMBL: AF170164; AAF89717.1; -.  
DR InterPro: IPR000345; CytC\_heme\_bind.  
DR InterPro: IPR002681; Iilar\_coat.  
DR Pfam: PF01787; Iilar\_coat; 1.  
DR PROSITE: PS00190; CYTOCHROME\_C; UNKNOWN\_1.  
SQ SEQUENCE 224 AA; 24882 MW; 5C2CCB6CF2AFBA71 CRC64;

Query Match 50.6%; Score 44; DB 12; Length 224;  
Best Local Similarity 60.0%; Pred. No. 7;  
Matches 9; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

QY 1 CASD GALVPRRLQHR 15  
| :||||| | | |  
Db 20 CHPNGALVPLRAQQR 34

## RESULT 13

Q9IMQ9 ID Q9IMQ9 PRELIMINARY; PRT; 224 AA.  
AC Q9IMQ9;  
DT 01-OCT-2000 (TrEMBLrel. 15, Created)  
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)  
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)  
DE CAPSID PROTEIN.  
GN CP.  
OS Prunus necrotic ringspot virus.  
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Bromoviridae;  
OC Iilarvirus.  
OX NCBI\_TaxID=37733;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN-PS 7/5A;  
RX MEDLINE=20349238; PubMed=10893149;  
RA Vaskova D., Petrzik K., Karesova R.;  
RT "Variability and molecular typing of the woody-tree infecting prunus  
RT necrotic ringspot Iilarvirus.";

RL Arch. Virol. 145:699-709(2000).  
 DR EMBL: AF170166; AAF89721.1; -.  
 DR InterPro; IPR000345; CytC\_heme\_bind.  
 DR InterPro; IPR002681; Ilar\_coat.  
 DR Pfam; PF01787; Ilar\_coat; 1.  
 DR PROSITE; PS00190; CYTOCHROME\_C; UNKNOWN\_1.  
 SQ SEQUENCE 224 AA; 24880 MW; 9401E4CEC3222B21 CRC64;

Query Match 50.6%; Score 44; DB 12; Length 224;  
 Best Local Similarity 60.0%; Pred. No. 7;  
 Matches 9; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

QY 1 CASDGLVPRRLQHR 15  
 | :||||| | | |  
 Db 20 CHPNGALVPLRAQR 34

RESULT 14  
 Q9IMQ7 PRELIMINARY; PRT; 224 AA.  
 AC Q9IMQ7;  
 DT 01-OCT-2000 (TREMBLrel. 15, Created)  
 DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)  
 DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)  
 DE CAPSID PROTEIN.  
 GN CP.  
 OS Prunus necrotic ringspot virus.  
 OC Viruses; ssRNA positive-strand viruses, no DNA stage; Bromoviridae;  
 OC Ilarvirus.  
 OX NCBI\_TaxID=37733;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-UHI;  
 RX MEDLINE-20349238; PubMed-10893149;  
 RA Vaskova D., Petrzik K., Karesova R.;  
 RT "Variability and molecular typing of the woody-tree infecting prunus  
 necrotic ringspot ilarvirus";  
 RL Arch. Virol. 145:699-709(2000).  
 DR EMBL; AF170167; AAF89723.1; -.  
 DR InterPro; IPR000345; CytC\_heme\_bind.  
 DR InterPro; IPR002681; Ilar\_coat.  
 DR Pfam; PF01787; Ilar\_coat; 1.  
 DR PROSITE; PS00190; CYTOCHROME\_C; UNKNOWN\_1.  
 SQ SEQUENCE 224 AA; 24879 MW; 28F24B0801EC4D7D CRC64;

Query Match 50.6%; Score 44; DB 12; Length 224;  
 Best Local Similarity 60.0%; Pred. No. 7;  
 Matches 9; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

QY 1 CASDGLVPRRLQHR 15  
 | :||||| | | |  
 Db 20 CHPNGALVPLRAQR 34

RESULT 15  
 Q9IMQ3 PRELIMINARY; PRT; 224 AA.  
 AC Q9IMQ3;  
 DT 01-OCT-2000 (TREMBLrel. 15, Created)  
 DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)  
 DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)  
 DE CAPSID PROTEIN.  
 GN CP.  
 OS Prunus necrotic ringspot virus.  
 OC Viruses; ssRNA positive-strand viruses, no DNA stage; Bromoviridae;  
 OC Ilarvirus.  
 OX NCBI\_TaxID=37733;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-NA HRBU;  
 RX MEDLINE-20349238; PubMed-10893149;

RA Vaskova D., Petrzik K., Karesova R.;  
 RT "Variability and molecular typing of the woody-tree infecting prunus  
 necrotic ringspot ilarvirus";  
 RL Arch. Virol. 145:699-709(2000).  
 DR EMBL; AF170170; AAF89729.1; -.  
 DR InterPro; IPR000345; CytC\_heme\_bind.  
 DR InterPro; IPR002681; Ilar\_coat.  
 DR Pfam; PF01787; Ilar\_coat; 1.  
 DR PROSITE; PS00190; CYTOCHROME\_C; UNKNOWN\_1.  
 SQ SEQUENCE 224 AA; 24863 MW; 2DE64B0811ED40A7 CRC64;

Query Match 50.6%; Score 44; DB 12; Length 224;  
 Best Local Similarity 60.0%; Pred. No. 7;  
 Matches 9; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

QY 1 CASDGLVPRRLQHR 15  
 | :||||| | | |  
 Db 20 CHPNGALVPLRAQR 34

Search completed: September 10, 2002, 10:46:25  
 Job time: 123 sec